# JUL 2 1 2006 W

# Docket No. CL001201DIV Application Serial No. 10/644,021 Inventors: Ming-Hui WEI et al. Title: ISOLATED HUMAN ENZYME PROTEIN...

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	1	GCGCCTGGGG	ACCGCAGAGG	TGAGAGTCGC	GCCCGGGAGT	CCGCCGCCTG
	51	CGCCAGGATG	GAGTTCGTGA	AATGCCTTGG	CCACCCGAA	GAGTTCTACA
	101	ACCTGGTGCG	CTTCCGGATC	GGGGGCAAGC	GGAAGGTGAT	GCCCAAGATG
	151	GACCAGGACT	CGCTCAGCAG	CAGCCTGAAA	ACTTGCTACA	AGTATCTCAA
	201	TCAGACCAGT	CGCAGTTTCG	CAGCTGTTAT	CCAGGCGCTG	GATGGGGAAA
	251	TGCGCAACGC	AGTGTGCATA	TTTTATCTGG	TTCTCCGAGC	TCTGGACACA
	301	CTGGAAGATG	ACATGACCAT	CAGTGTGGAA	AAGAAGGTCC	CGCTGTTACA
	351	CAACTTTCAC	TCTTTCCTTT	ACCAACCAGA	CTGGCGGTTC	ATGGAGAGCA
	401	AGGAGAAGGA	TCGCCAGGTG	CTGGAGGACT	TCCCAACGTA	CTGCCACTAT
	451	GTTGCTGGGC	TGGTCGGAAT	TGGCCTTTCC	CGTCTTTTCT	CAGCCTCAGA
	501	GTTTGAAGAC	CCCTTAGTTG	GTGAAGATAC	AGAACGTGCC	AACTCTATGG
	551	GCCTGTTTCT	GCAGAAAACA	AACATCATCC	GTGACTATCT	GGAAGACCAG
	601	CAAGGAGGAA	GAGAGTTCTG	GCCTCAAGAG	GTTTGGAGCA	GGTATGTTAA
	651	GAAGTTAGGG	GATTTTGCTA	AGCCGGAGAA	TATTGACTTG	GCCGTGCAGT
	701	GCCTGAATGA	ACTTATAACC	AATGCACTGC	ACCACATCCC	AGATGTCATC
	751	ACCTACCTTT	CGAGACTCAG	AAACCAGAGT	GTGTTTAACT	TCTGTGCTAT
	801	TCCACAGGTG	ATGGCCATTG	CCACTTTGGC	TGCCTGTTAT	AATAACCAGC
	851	AGGTGTTCAA	AGGGGCAGTG	AAGATTCGGA	AAGGGCAAGC	AGTGACCCTC
	901	ATGATGGATG	CCACCAATAT	GCCAGCTGTC	AAAGCCATCA	TATATCAGTA
	951	TATGGAAGAG	ATTTATCATA	GAATCCCCGA	CTCAGACCCA	TCTTCTAGCA
	1001	AAACAAGGCA	GATCATCTCC	ACCATCCGGA	CGCAGAATCT	TCCCAACTGT
	1051	CAGCTGATTT	CCCGAAGCCA	CTACTCCCCC	ATCTACCTGT	CGTTTGTCAT
	1101	GCTTTTGGCT	GCCCTGAGCT	GGCAGTACCT	GACCACTCTC	TCCCAGGTAA
	1151	CAGAAGACTA	TGTTCAGACT	GGAGAACACT	GATCCCAAAT	TTGTCCATAG
	1201	CTGAAGTCCA	CCATAAAGTG	GATTTACTTT	TTTTCTTTAA	GGATGGATGT
	1251	TGTGTTCTCT	TTATTTTTTT	CCTACTACTT	TAATCCCTAA	AAGAACGCTG
	1301	TGTGGCTGGG	ACCTTTAGGA	AAGTGAAATG	CAGGTGAGAA	GAACCTAAAC
	1351	ATGAAAGGAA	AGGGTGCCTC	ATCCCAGCAA	CCTGTCCTTG	TGGGTGATGA
	1401	TCACTGTGCT	GCTTGCGGCT	CATGGCAGAG	CATTCAGTGC	CACGGTTTAG
	1451	GTGAAGTCGC	TGCATATGTG	ACTGTCATGA	GATCCTACTT	AGTATGATCC
	1501	TGGCTAGAAT	GATAATTAAA	AGTATTTAAT	TTGAAAAAAA	AAAAAAAAA
	1551	AAAAAAAAA	AAAAAAAAA	AAAAAAAAA	AAAAAAAAA	AAAAAAAAA
	1601	AAAAAA (SE	EQ ID NO:1)			

#### FEATURES:

5'UTR: 1-57 Start Codon: 58 Stop Codon: 1180 3'UTR: 1183

#### Homologous proteins:

Top 10 BLAST Hits

·	Score	E
CRA 108000024649260 /altid=gi 12734163 /def=ref XP_005134.2  fa	770	0.0
CRA 18000004925908 /altid=gi 4758350 /def=ref NP_004453.1  farn	743	0.0
CRA 18000004929946 /altid=gi 2135096 /def=pir  I38245 farnesyl	741	0.0
CRA 18000004993865 /altid=gi 2136196 /def=pir  I52090 squalene	740	0.0
CRA 18000004932414 /altid=gi 6753838 /def=ref NP_034321.1  farn	671	0.0
CRA 18000004937535 /altid=gi 9506591 /def=ref NP_062111.1  farn	654	0.0
CRA 1000682330885 /altid=gi 6002565 /def=gb AAF00038.1  (AF0903	582	e-165
CRA 335001098694081 /altid=gi 11514495 /def=pdb 1EZF A Chain A,	579	e-164
CRA 18000005103884 /altid=gi 2463565 /def=dbj BAA22557.1  (AB00	282	1e-74
CRA 18000005103885 /altid=qi 7434086 /def=pir  T00489 farnesyl	280	4e-74

#### BLAST dbEST hits:

	Score	E
gi 12926380 /dataset=dbest /taxon=960	1441	0.0
gi 12945082 /dataset=dbest /taxon=960	1370	0.0
gi 12921315 /dataset=dbest /taxon=960	1346	0.0
gi 11642571 /dataset=dbest /taxon=96	1330	0.0
gi 9141948 /dataset=dbest /taxon=9606	1281	0.0
gi 13040072 /dataset=dbest /taxon=960	1233	0.0
gi 12944143 /dataset=dbest /taxon=960	1055	0.0

#### EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|12926380 placenta gi|12945082 T cells from T cell leukemia

gi|12921315 Fetal brain

gi|11642571pancreas

gi|9141948 Burkitt lymphoma

gi|13040072 bladder

From tissue screening panels: . Whole liver

1 MEFVKCLGHP EEFYNLVRFR IGGKRKVMPK MDQDSLSSSL KTCYKYLNQT
51 SRSFAAVIQA LDGEMRNAVC IFYLVLRALD TLEDDMTISV EKKVPLLHNF
101 HSFLYQPDWR FMESKEKDRQ VLEDFPTYCH YVAGLVGIGL SRLFSASEFE
151 DPLVGEDTER ANSMGLFLQK TNIIRDYLED QQGGREFWPQ EVWSRYVKKL
201 GDFAKPENID LAVQCLNELI TNALHHIPDV ITYLSRLRNQ SVFNFCAIPQ
251 VMAIATLAAC YNNQQVFKGA VKIRKGQAVT LMMDATNMPA VKAIIYQYME
301 EIYHRIPDSD PSSSKTRQII STIRTQNLPN CQLISRSHYS PIYLSFVMLL
351 AALSWQYLTT LSQVTEDYVQ TGEH (SEQ ID NO:2)

#### FEATURES:

#### Functional domains and key regions:

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION N-glycosylation site

Number of matches: 2

- 1 48-51 NQTS (residues 48-51 of SEQ ID NO:2) 2 239-242 NQSV (residues 239-242 of SEQ ID NO:2)
- [2] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site

Number of matches: 5

- 1 39-41 SLK
- 2 50-52 TSR
- 3 158-160 TER
- 4 313-315 SSK
- 5 322-324 TIR
- [3] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site

Number of matches: 3

- 1 81-84 TLED (residues 81-84 of SEQ ID NO:2) 2 145-148 SASE (residues 145-148 of SEQ ID NO:2) 3 147-150 SEFE (residues 147-150 of SEQ ID NO:2)
- [4] PDOC00008 PS00008 MYRISTYL N-myristoylation site

Number of matches: 2

- 1 137-142 GIGLSR (residues 137-142 of SEQ ID NO:2) 2 276-281 GQAVTL (residues 276-281 of SEQ ID NO:2)
- [5] PDOC00009 PS00009 AMIDATION Amidation site

22-25 GGKR (residues 22-25 of SEQ ID NO:2)

[6] PDOC00802 PS01044 SQUALEN\_PHYTOEN\_SYN\_1 Squalene and phytoene synthases signature 1

128-143 YCHYVAGLVGIGLSRL (residues 128-143 of SEQ ID NO:2)

[7] PDOC00802 PS01045 SQUALEN\_PHYTOEN\_SYN\_2 Squalene and phytoene synthases signature 2

164-189 MGLFLQKTNIIRDYLEDQQGGREFWP (residues 164-189 of SEQ ID NO:2)

Membrane	spanr	ing str	ucture	and domains:	
Helix	Begin	End	Score	Certainty	
1	125	145	0.834	Putative	
2	241	261	1.467	Certain	
3	339	359	1.716	Certain	

#### BLAST Alignment to Top Hit: >CRA|18000004925908 /altid=gi|4758350 /def=ref|NP 004453.1| farnesyl-diphosphate farnesyltransferase 1; Farnesyl-diphosphate farnesyltransferase 1 (squalene synthase); Squalene synthase [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=417 Length = 417Score = 743 bits (1898), Expect = 0.0Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%) MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60 Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA Sbjct: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60 Query: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ Sbjct: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120 Query: 121 VLEDFPT-------YCHYVAGLVG 137 YCHYVAGLVG VLEDFPT Sbjct: 121 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180 Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV 197 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV 240 Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257 $\tt KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL$ Sbjct: 241 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 300 Query: 258 AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR 317 AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR Sbjct: 301 AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR 360 Query: 318 QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH 374 (SEQ ID NO:2) QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH Sbjct: 361 QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH 417 (SEQ ID NO:4) >CRA|108000024649260 /altid=gi|12734163 /def=ref|XP\_005134.2| farnesyl-diphosphate farnesyltransferase 1 [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=431 Length = 431Score = 743 bits (1898), Expect = 0.0 Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%) MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60 Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDODSLSSSLKTCYKYLNOTSRSFAAVIOA Sbjct: 15 MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 74 Query: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ Sbjct: 75 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 134 Query: 121 VLEDFPT------YCHYVAGLVG 137

#### FIGURE 2C

Sbjct: 135 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 194

YCHYVAGLVG

		THE TOTAL TOTAL THE TROPERS
Query:	138	IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV 197 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV
Sbjct:	195	IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV 254
Query:	198	KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL
Sbjct:	255	KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 314
Query:	258	AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR 317 AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR
Sbjct:	315	AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR 374
_		QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH 374 (SEQ ID NO:2) QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH
Sbjct:	375	QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH 431 (SEQ ID NO:5)
>CRA 1		004929946 /altid=gi 2135096 /def=pir  I38245 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21), hepatic - human /org=human /taxon=9606 /dataset=nraa /length=417 Length = 417
Score Ident	= itie	741 bits (1893), Expect = 0.0 s = 373/417 (89%), Positives = 373/417 (89%), Gaps = 43/417 (10%)
Query:	1	MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60 MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA
Sbjct:	1	MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60
Query:		LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct:		LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
_		VLEDFPTYCHYVAGLVG 137 VLEDFPT YCHYVAGLVG
-		VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180
_		IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV 197 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV
-		IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV 240
-		KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL
-		KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 300 .
		AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR 317 AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR
		AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR 360
~ 1		QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH 374 (SEQ ID NO:2) QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYL TLSQVTEDYVQTGEH
Sbjct:	361	QIISTIRTQNLPNCQLISRSHYSPIYLSFVMLLAALSWQYLATLSQVTEDYVQTGEH 417 (SEQ ID NO:6)

#### Hmmer search results (Pfam):

Model	Description	Score	E-value	Ν.
PF00494	Squalene and phytoene synthases	425.8	4e-124	2

#### Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF00494	1/2	47	126	• •	1	88	[.	124.6	1.1e-33
PF00494	2/2	127	291		146	317	.]	301.1	1.3e-86

1 TATTTATTCC TAATTAAATG GGGAGGAAAG TCTTTGAAGA GGAACCTCTA 51 CTTTACTTTT TATACCGTCA TGGCTGGAAA CTAAGTTTTT AAGATTTTTC 101 TGGGGTTCCC TTGGCCGAGG TGGGGAGTGG GAGGGCTGTC CAGTGGTAGG 151 GACTTAGGAT TTTTAGTTTA CAGTAGTAGG GGAAACACTC TGTAATCTAA 201 TACATAAGTA AATGATGTAT TAGAATATGG TAAATATAGG CAAGTAGACC 251 CCCACTGGGA TTAGCAGTGG TGGAAATGTG AGAGAGGGCA AACAGGTGGG 301 TCTAGATGAG GTGTGAGCAG ACTCGAGGGG CACAGGAGTT AGTCAAGCCA 351 GTATCTGGGG GATAGTGCAG GAATAGTGAA CAGCTAGACA AAAAGTCCTA 401 GGGCCAGAGA AAGCAAAAGC ATAAGAGATG GAGGCCAGAG AGGTAATCTG 451 GGTGGAAGGC TGCAGCCTCT CAGGATCCCT ATAGGTGCTT TGGCTTTTGT 501 TGGAGAGACA CTGAACAGCT TTGGGCAGTG AACGTACCTG ACAGGTTTCC 551 TGTTTGTTTT TGAGATGAAG TCTCGCTCTT GTCCCCCAGG CTGGAGTGCA 601 ATAGCGCGAT CTCAGCTCAC TGCAACCTCT GCCTCCTGTG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCA GGTAGCTGGG ATTATAGGCG CCTGCCACCA 701 TGCCTGGCTA ATTTTTGTAT TTTTAGTAGA GACGCAGTTT CAGCATGTTG 751 GCCAGGCTGG TCTTGAACTC CAGACCTCAG GTGATCCGCC CGCCTTGGCC 801 TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCGCTC GGCTAGACCT 851 GACAGGTTTT AAAAGGATTA CTGGTTGCTG TGTTAAAACA GACTGCAGGA 901 TGGCTTAGGT AGCCAGTAGG TTTTTTTTT TTTTGGAGAC GTAGTCTTGC 951 TCTGTTGGCC TGGCTGGAGT GCAGCGGTGT CATCTTGGCT CACTGCAAAC 1001 TCCGCTTCCC GGGTTCAAGT GATTCTCCTG CCTCAGCCTC CGGAGTAGTT 1051 GGGACTACAG GCGCCCACCA CCACACTCGG CTTTTTTGTA TTTTTAGTAG 1101 AGACGGGTTT CACCATGTTG GCCAGGATGG TCTCGATCTC TTGACCTCGT 1151 GATCCACCCG CCTTGGCCTC CCAAAGTGTT GCGATTACAG GCGTGAGCCA 1201 CCACGCCTGG ACGGGTAGCC AGTAGTTTCT AGGGCTGGAG AGATCTAGGA 1251 TGAGAGAAGT TTCCACATTC CTGTTACAGG CTCTCTAAGG CTTCAGCTCC 1301 TTTTTCTAGG ACTAAGCTGG ATCTCAAGTA AACACTAGAG AGGGGGCAGC 1351 TGAAGCTCCA GGAGTGTGTG GGGCTCCCTG GGGCTGGATG GCGGTGGCGG 1401 GCAGGCGAGC TGGGCTGTGC TCGGGTGTGT TACAGTAAAG ACGCCCAGCT 1451 TGGCGCTGGC CCGGCCTTTT CACGGTTTTA GGCTCTACAG AGAGCGGCTG 1501 CAGAGCTCAC CCGGCTGGCA GGAGCCACCG AGGCCGGACA CGTGGGCGAC 1551 TTATTGACCA AGTGGGGAGG AAGCAGCCCC GCACTGCTCT CCCGACTGCG 1601 GACCACCGTT GGGCTCATGC GCATCATAAG CCCCACCGCC TCACCTCCAG 1651 TCCCCACAGC GTTCGCGCTC CCAGCCGGGG TAAGCGGAAG AAAACAAAGG 1701 CCCGGCTCCA TCAGGGCACC AATCCCGCTC GTCGGCCTCT TTCTCGGCCT 1751 CCAATGAGCT TCTAGGGTGT TATCACGCCA GTCTCCTTCC GCGACTGATT 1801 GGCCGGGGTC TTCCTAGTGT GAGCGGCCCT GGCCAATCAG GCGCCCGTCA 1851 GCCCACCCA CGAGGCCGCA GCTAGCCCCG CTGGCGGCCG AGGCCGGTTG 1901 AAGTGGGCGG AGCGGCGGGC GGGGCGTCGC CGTACTAGGC CTGCCCCCTG 1951 TCCGGCCAGC CCCTCGAAGC ACCTACTCCA CAGGTCCAGC CGGCCGGTGA 2001 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCCTG 2051 CGCCAGGATG GAGTTCGTGA AATGCCTTGG CCACCCCGAA GAGTTCTACA 2101 ACCTGGTGCG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG 2201 CTGGGCCGGC CTCAGGGCCT GAGCGGCCGG GCCCGGATCT GGGGCAAGGG 2251 GCGCGGCGAG CAGGGCCGAC GCCTGGGTGT TCCCGTCCCC CTTTCCTCGA 2301 GCCTTCCCCC TGTAGGGCCC GGGTGGACGC GGCCGTCCTG GCTGACCTGT 2351 CCCTGCCCC GCAAGCCGCC CTGGGCATGA GCGACTTTTG CGTGGTTCCC 2401 GGTGGTTGCG CTCCCCGTTT CGTCCCCTCC GTGAGCATCG GCGCTTACCG 2451 GTATTTTAAC CCGAGGGTTA CACATCTGAG GCAATGTGGG TGGGTTACGC 2501 GGGAGAGGAC GAGTGAGTTT TTTGGTAAGC GGAATGAACT ATGCAGATAA 2551 CATCACATGA AGGCCGTTTC TGGAATGAAG TCTGACTCCT CCAGTTTCAC 2601 CACCTCTTCC GGAGCTCTCC CCGCCTTGCT GCCTTCCATC GCTTCATCCT 2651 CGGTGCTTCC TGAGTTTTAA AATCGCCTAT CTACGCTTCC AAGTTCCAAT 2701 GAGTTATCTA ACGTCTATGG ATTAGCTAGG TGGTTGGTGG AAGGTCAGAA 2751 CTTGGTTTTA CTTAGATTTT TATCTGCCTC ATGCCTGTAC TATTTGTTTA 2801 ATGAATGCAT AGGAGGTGTT TTTATTCCAA CAAGAAAATT ATTCGTACGC 2851 GATTATTGAA TGAATAGACA AATTCAGCCA AGTTCTTCTG GTCTGGACCA 2901 GCCTGGCTGA TTTCTGTAAC TTTTTTGGGC CAACAGGACA GTAGCAAATG 2951 TGACTCAGGC CGAGGCTTGA TAGGTGCCTG AACATCGGAG TCTTTCTTTC 3001 AGTGTCCATG TGCTTCAGTA AACACACTAG AAAATAAATT TCTGGTTTTT 3051 GTCCCCAGTA GACTACACCC TCATTTGGTG TTATTTTTCA CGTGCTATCT.

3101 TTAATACAGG TACATCCTTC AGTCTATTTG TAGAACATTC AGTTTTCTTC 3151 ATCTTTCTT TGCCGGTGCT ACATTATTTG AATTATTTTG CTACAGAATA 3201 ACTTCTATTA TTTGATATGG CAGATGTCAC TTTTTATATT TAGATATAGC 3251 ATTCATTTAT TTAACAAATA TTTGACGACC AGTTGTATAT CAGATAGTGT 3301 TCTAGGTGCT GGAGGTACAA CAGTGAACAA GCTAGGTGAA GACCTTGATT 3351 TTATAAAACT TACTTTTTAG TGGAAGAGA ACAATTTAAA AAAGCGAATG 3401 TACAGTTTTT CACGTGGAGA AAAGCACTGC AGAGGAAGAT ACTAGCAGGG 3451 CAAGGGATCT GAGTGCAGTC AGACCTCATT TGGGTCCAGA CTTCATTCCT 3501 CTATGTCTCT TTCCTTTCTA CAGAAAGACT GTTAGAGAAA ATGGTAGCAT 3551 TGGTTTCCTG TTGGGAGGGA AAGTGGGTGG TCATGGTAAG TGGGTAGAGA 3601 AAGACTTCAC AGTATACTGT TTTTGTACAT TTTGAGTTTT TTTAAAAGCG 3651 AGACTTGAGC TATTCTAGCT CTGATAATAT GGTGCAGTAT TTGTTATGTT 3701 AGTTGTAGTC TTTCTGGGCA GTTTTTACAT CCCCATGAGC CGTTAAAAAA 3751 ATACCTGAAC CTTTAATTAG GGGAAATAAA TTGGAAAAAT ACATTTCCCT 3801 TCACTTAACA TTATCTTAGT TTCTCTTTTT TTTTTTTTT TTTTTTGAGA 3851 TGGAGTCTTG CTCTGTTACC CAGGCTGGAG TGCAGTGGTG GCGGGACCTC 3901 AGCTAGATGC AGCCTCCGCC TCCTGGGTTC AAGCAATTCT CCTGCCTCAG 3951 CCTGCTGAGT AGCTGGGATT ACAGGCACCT GCCACTACGC CCGGCTGATT 4001 TTTTGGTATT TTTAGTAGAG ACGGGGTTTC ACCATGTTGG CGAGGCTGGT 4051 TTTGAACTCT TGACCTCAAG TGATCTGCTC GCCTTGGTCT CCCAAAGTGC 4101 TAGGATTACA GGCGTGAGCC ACTGCACCCG GCCTTTTTTT TTTTTTTTT 4151 GAGGGGGGG TCTCACTCCA TCGTCCAGGC TAGAATGCTG TGGCCTGAAC 4201 ATGACTCACT CCAGTTTTGA CTTCCTTGGC TGAAGCCATC CTCCCACCTC 4251 GGCTTCCTGA TCCCGAGTAG CTGGGACTCC AGGCACGTGT CACCAATGCA 4301 TGGCTAATTT TTAAATTTTT TTGTAGACAC AATGTCTCGC TGCATTGCCC 4351 AGGCTGGTCT TGAACTCCTG AGCTCAAGCG ATTTTCCCAC CTCAGCCTTC 4401 AAAGTGCTGG GATTACAGGT GTGAGCCACT GCACCCAACC AGTTTCTCTC 4451 TGCAAACTAG GGAAAAATT TACGCTTAGC AGATATTGAG GGCTGATTAT 4501 TTCTATCACA GAAGCATTTG GCTATAGAAT TTCAGGGTTT AGTAAACTTG 4551 ATTTACACTG AATTTTTAGG TGCATATCAG TAAATCTACG GGCATATGCC 4601 GCCTGCAAGT TGTGTGGCAT CACCCAAAAG CCGAGAGTAA TGGAAAGAGC 4651 AGGCTGTTAG TAATCAGGCA GATCTGGCTC CTGTCCAATC TAAATCCTGT 4701 TATTTAGACT AATATCTTAA GTCTGTTATT AAGTCCGATT TCTGACGCTA 4751 TTAAGTTAGG TGAACAACCT TGGTAACTTA ACCTCTGAAC CACAGTTACT 4801 TCATCTGTAA AATAGGGATG TATGTATGGT AACGATTTTT TAACCACAAC 4851 TTCCCAACTC TAAGATGGTC TGAAAAGAAT TTTTTGAGTG TTTGGCTCAG 4901 AATCACTTGG CAGCAAAACC TGACTTGAAG TTGAGGCTTC ATTCATCCCA 4951 CTTAGTATAT TCAAATGTTT TGCTAAAGAA ATAATTATGA GGTGCTACTT 5001 CACACTGACT AGGGTTGTAT ATGCATTTTA TTGCCTATTT TCTAAAACAC 5051 TAAAAATGCT AAATTCTGCC CCAGGTCTTG CCACAGATGT TTCAGTGGAC 5101 TATGGGCCTG TGAGACCTTA AAGGGTTGAT TGAGTAAGGA TCACAGGTGA 5151 TGTCCGCATT GTGCTTGGCA TGGAGTTAAG TGCTTGATAA ATGGTGGTTA 5201 TCAATCTGAT TATGTAAATT TATGTAAATT CAGTTCTCAA GTTTGTGGTT 5251 TTTTTCCCCT CCTGGAGAAA TCTATTCTAT TTTAAAGTGA GGAAGGCTCC 5301 GTGGAGGGCT GGTAGCTGGT AGCTGTTCAC TTGTGGAACT TTCAGCCTGA 5351 GGCTGGAGCC CCTTCCTGGG AGTCTGGTCT TGTCGTCTTC CTGACCACCC 5401 CCACACCCTT CCTCTAAATT CCCTCCATCC CTGTTTTTCT CCCGCTTGCG 5451 AGCTTTTGGG AGTGTGCTGA ATCTCAGACT GCAATAGATA AACCCAAGAG 5501 GGACAGGCAC CAGTAGCCTG AGCTTGCTTT CTCCCCTGGC TCATGGGAAT 5551 CAAGCAGTAG AAATTTTTAG TGAGTGTTGT TTTCCATAGT ATGCTTACTA 5601 GTTGTGTCTT CCTGTTTTGT TCTTGGTGAT TTGAAGAAAC CTGTTTACAA 5651 GGTAAGGGAC TGAAACAAAT AGGTGACAGG AAAAAGAGCA GCAGGGGTAC 5701 GAGCTGGAGG AGTAAGTGGC TTGGCTTGCT CTCTTTCAGA ATGGAGGGCT 5751 GTATGGAAAG GAGGGGTAGT GTTCTTGAAG AGTGTTGGGG TTTAAATCTA 5801 GGGGGACCGT GTCTTGGCAT TGATTGAAAC TCCTGGCTTA ACATCACCCC 5851 GAAACTGTTA GTTGGACTGA ACATGACATT TGGCAGTGCA GTTAAAAACA 5901 CTTCCTGCTG TAGCCTGGTA ATGGTCAGGC TATGTGAAGA GCTGCTCTGG 5951 AGCTCAGTCC AGAGCGGGTA TTCTGTTTCT TTCACTCTGA AATCCTGCCT 6001 CTCGATATTT TGAGAAGGAA GGAGTTGGTG AATTGTTTTA AAATCCTCGA 6051 TGAATGTCTT CATTTATTCA TGACACCACT TCTGAATATA TTTATGTGCC 6101 AGACGCTGAA GTTTACTAAT ATTATGGTGC CCAGTAAATA CTTGTTTTTA · 6151 CTAATATTT TTATGGCAAT AAAATGACTT TTTCAGGATT ATGTGATTTA

6201 AAAGATTGAC CCTTTTGGCA AAATACGTAT TCATGATAGG AAATATATAC 6251 AACATAGTTC ACTTAAACCT CCCACCAGAG CCCAGGGTTC ACTGTTACCA 6301 TTCTGAAGTG ACTGGAATTT CCTAGAAGTG GATATGCCAT ATTTTTTTAA 6351 CCACTCCTAT TGGATATTTG TTTTTATTT TTTTGAGATG GGGTCCCACT 6401 CTGCAGTGTA CAATATCATA GTTCACTGTA ACGTGTATCT CTTGGGCTCA ·6451 AGCGATCCTC CCCACCTCAG CCTCCCTGAG TAGCTAGTCT TCAGTAGCTA 6501 GACTATAGGT GGGCGCCACC ACAGCTGGCT TTTTAAAAAA TTTTTTATGA 6551 ACACGAGGTC TCACTATGTT GCCCAGGCTG CCCTCAAACT CCTGGGCTCA 6601 AGTGATTCTC CCACCTTGGC CTTCCGAAGT GCAGGGATTA TAGGCGTGCG 6651 CCACTGCACC CGGCCCTGTT GGATAAATGA TTCCAGTCTC TCCCAAAAAG 6701 AACTGTTGTA AGACTGTGGG GTGAGGGGAG GGAAGGGACA AATAGGAACC 6751 CGCCGTATTT TCCACTCCT GTGGGCCTAA AACTGCTCTA AAAAATAGTC 6801 CATGAAAAA TACATAGTAC AAACAGCAAC TCTTTCTGAT ATGCTTGCAT 6851 TTAAAATCAG GCTTTTTCTC CCTTTTGGAA AAACACAGTC CTTGTTTGCT 6901 TTAGGGAAGA GTAAAGGTCA GTGCGCTGCA TTGCATTAAT TTCGAAGGGA 6951 AAGATGAGAA GACATCTTGA AAGGAATGGC TGGCTTTCTA GAGAATAGTA 7001 GAGGCTTAAT AGGTGTCATA GAAAAACCAG GGTTGGACAG TGGTAGTAAA 7051 ACGGCAAAAC AGATTTTATT CAGAAAAACT ACTGCAGTAA GAGGAGAGAG 7101 ACCTCGGTAC AGAACTGCTC CACTGCGAAT ACAAAGAAAA GTAGGAATTG 7151 ATGGCGGGG AGCCGGATGT CAGTGGATGG AAAATTATTA CGAGGAAACA 7201 CAGGGGTGTG CATTCTTGCT GAAGGCAGGC CAGAGTTATC AGACATCACC 7251 TGAGGGATGG AGGGGGATGT GGAACCTAAT CGGCTGTCTA GGGTGATCAG 7301 ATACTGAAGT TGGGGGATTC TGGTCAAATC AATTTAGCAG GATTCTTGGT 7351 AAAACTGGGC GATGCAAAGA CAGATGCGTT GAGTACAAAG TCCAGGCTTT 7401 ATTGGGAAGA GGATTTCAGC GGAGCCCGAG TAGAGTTTGG TCTAGGGAGA 7451 CTCTGTCACT GGGAGGACGA GCGAGCCGCT CGGAAGTGCG .CTGGGTTCTC 7501 TTAGCGGCCA GTGGGTTCTG GTGAGAAGGG CAACAGCGGG AGGAGGCGCC 7551 GGTGCGGAGC GGGAGGCCGG GGGCGGGCT GCGGGGCTGC GGGGCGGGCC 7601 CGTTGTGGGT CGGCCCAGCG CGTATTCGAG TAGAGGGCGA GCCCGTCCCG 7651 CCTCTCGTCG GGCGCTTCCC AGATCTGCTT GAGTCTATGG AGGAAAAACT 7701 CCGCGGGGTC CGCGATTCCC ATGGCCGCAG CCGCCTGCGG CACCAAGGCC 7751 ATGGCCCTCT TCAAGCGCAC CTTGGTGCTG AGTCCCGCCG CGGCGCCCAG 7801 GGGCCCGGGC GCAGGCACCG CCCCGCGGGG CTGCTGCTTG CCTCCTGCCG 7851 CCTGGCCCTG CAAGGACTGG CCTCGGGGAG AGGGCGGCAG GCTGTGGAGC 7901 CGCCTGCCCC AGTCCCAGTC CCACTCCCAC TCCCACTCC ACTCCCACTC 7951 CTGCTCCTCG ACGTCTCCCA CCGCCGTGTG TGTTGTCTGC CCGCAGGACT 8001 CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA TCAGACCAGT 8051 CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGGAAA TGCGGTGAGT 8101 GATGGAGGCA GCGCCTCTGG CTTGGAGGAA AGCTTGTCCG GGACTTTTGA 8151 GTGTGTTGGA AGCTACCTTT TGATATAGCG CTCAGCGTTG CAGCCTCGTT 8201 GCTGTGGCTT ATCCAGAACA TAGCCCGGCC CTACGTGTTT ACTTTAGAAA 8251 GCCCTTCCAG GCTCTTTGCC ATCTAGTAGA GTCCCTGCGG GCCCAGCCTT 8301 TCAGAGAAGG GGGGGGAGGG GGTGATGTTT ATTAACTTTT TTTAGTCTTG 8351 GCAGCTGAAC CTGCCTGTGA GCAGGTCGTG TATTTCTCGG CTTCCCTTAT 8401 CCAACTTTGC ATTTCTATTT CTAGCATATT GGGTTGATTC TTTTGAAGCT 8451 GCCTCTGTGC ACATTACACC CATGAACTTA GACCAGTTGC CTTTATGTAT 8501 GATCGTATTT ATACTGAGAA GTTACTGTGT TTTTTGACTT TCTTTTCTAT 8551 TTGCTACATA TTAGTTCGGT CTAAACGTTT GGTCTTCTGG TCTCCATAGT 8601 TCTACATTGG TTAAATGCAA CTCACTTCTG GGAGTAGTGG TGACATTCAA 8651 CTAGTAGGCT TTTTAATAAA CTACAGAAGT TCATTACTCT CATGTAAGGA 8701 AGGAAAACTA ATGTAACTTT CGTTAAGTAT GAAAAGCGTT GGATATCCTT 8751 ATAGTTCTTT AGAGTTAAGG GTGAGATGGG TTTAGAAAGT GGCCAGGCAC 8801 AAGTTATTTT AAAATAAAA ATCTTTGGCT GTTTGTTCCA ATATATTAAT 8851 AGTTTTCCCT TTTTTACAGC AACGCAGTGT GCATATTTTA TCTGGTTCTC 8901 CGAGCTCTGG ACACACTGGA AGATGACATG ACCATCAGTG TGGAAAAGAA 8951 GGTCCCGCTG TTACACAACT TTCACTCTTT CCTTTACCAA CCAGACTGGC 9001 GGTTCATGGA GAGCAAGGAG AAGGATCGCC AGGTGCTGGA GGACTTCCCA 9051 ACGGTGAGTG GGGTTACGCA TCTTGTCTAC GGACTGTTGT GTTCATAATT 9101 GCTAACGTGG TTGTCCGGTA GCCTCCATAC ATGTGGAGAA AGGTTAAATA 9151 AGCATTCTGA GGGCAGCATA ATGTGAGGGT TAAAAACTCC GGTAGCCAAG 9201 ACTCTGAAGC CAGGCTGCCT GGGTTGGAAT CTCAAATCTC CCACTTACTA 9251 AACTGTTGGT TACTTACAAA GACTCTCTGT GCCTCAGTTT CTTCATCTGT

9301 AAAATAGGGG TAATAATAAC ACCTACCTCA TGGTATTCTG AGGATTCAAA 9351 GAATTAACGT AGGTAATGCT CTTAGAATGT TAGCTACTGC TGTTATTATC 9401 AGTATTGGAA GTCCAGTGTT TCTTCCTGTG GGAAGACGCA GTCAAATTTT 9451 AGTGTTGTGA AAGATTCTCA GGCTAGCTCA CAAAAGCCTG CCGACTGTAT 9501 GATGCAGCCT ACCTGTAACA CTGCTGGCCT CTTGACTACC CGGAGCCTGG 9551 TAGCATGGGA CTGCTGCTCA CGATGGGCAG CAGCCTGGCA TGGGGGCGGT 9601 GTCTGTTGGC AGCTAGGGCG AGCCTCTGCC ACTTCACCTG TGATCCTGGG 9651 CAAGTTCCTT ATCTGCTTTG TGTCTCCGTC TCCTCGTTTG TAAAGTTAGA 9701 GCTGAGAGGA TTAATTTCGC ACATATAAAG TACTTAGTGC CTGGTACAGG 9751 GTAAGTATTC TGTAAGTATT AGCTATTTGG TCTATTTTGT TGGAGTAAAG 9801 TGGGTTATAG TTAAAATCCT AAGATTTTTA AAGTCCCTCA AGTTCACGTG 9851 GACATCTGCC TAGGTCCTAC TATCCTAGAA TTCGCATGTC TTATCACACA 9901 AATAACTGAT TCTTCCATAT CTTATAAATA AAGGTTTGAT TTAGCAAAGT 9951 CACATGTTGT GTAATAGCTC GAAGAAGCCC TTTTTGTCCA CAGTTGCCAG 10001 AGCTTTTGGA GAACAGTCCT TATGTTATTG AAACAAACCT AATCTGTAGC 10051 TGAGTTGGGA GGGAGCTAAG TGGACAGAGA GTCCTCCACC CAAACAAAAG 10101 AATCTTTGAT TCTTGGGCAT AATGGGAGCA ATATTTAAAA AAAAAAAAA 10151 AAAAAAAAA GGAATGTTTG GGGAAGACTC TTGCGGTGCA AAGGCTGTTT 10201 CAGATTGCTG AGATCAGACC TTAAGTACCA AAGCCCAAAT ATAGTACAAC 10251 ATAATACAAA TGAGAAGAAA ATAGCTGAAG AATAATTCGA GTTTATACAG 10301 TACAATTCAA GAGAAGAAAG AAAATTTATG ACGACTAGCT GGGTGAGAAT 10351 TAGAACTGTA ACCCTGGGAA GGTCCTGGTG ATTTGACTCT CACAGGACAC 10401 CTGATGACCA GAGGATGGGT TTCCTTTGAT GGGAAATCTG TGGCGATTCA 10451 TTGATGGCC TCTGAATTCT GCTGAAGCAG AGGAAGTAGT AATACCCCAT 10501 TTATAATGGA AGTGCATTCT CACTTAAAAA CAACTAATAT TATTCTAGCT 10551 GGACCTAGCC TCTAGAAACA GCCAAATTAC ATTTGACTTG AGTGGATTCA 10601 TAATAATTAA AAAATTTCTG GGGCATGGGA TAAATGTGTT AGGTATTGCT 10651 AAGTCAAGGC AGCCCTATCC CCTCAGCAGA AGTGAGGGAA TATGAAAGTG 10701 TGTGAATGCT AACATAATTT TGGGGAATAT CGCCGTCAGA TTTCCAGATG 10751 ATATTCCAAC ATGTTTGTGA AACTTCAGTG TCTTCCTGTG TTCATACAGT 10801 GTTCCAGTGG AAAAATAATG CTTAGTTCTG GAAGGTTTCA GATGTGAACA 10851 CTGAACTCAT CGTTTTCTTT TTTGGGTAGT AGAGTTAGAG ATTCCATCCT 10901 CTTGAAAGCA CAGTTGCCCC GGGAAGAGTA AAAGGGAGCA GAAGGCGTAA 10951 GCCAGGCACG GCTGTTTTCA CTGTTGTTCA CCTTTTGTAT CCTTACGAAT 11001 ATGAAGATGT ACTAAGTTGT GTGTTTTGCG TGCATATATA ATTTTAAGCT 11051 ACTTGAGTTG TAGGTCCCTC CAGTCTGTGA TTCAGTTTGA GATGGGACTG 11101 TATGGGAATT AACAGTGCCT TGTCTTCTTA AGCAGTGATT TGTGTATGTG 11151 CTGATATAGC TCAGTATGTC TTTGAAACCA GTTGTCTGGG GCTAGGCCTG 11201 CAATCAGCTT TTGGCTAAGA GGTCCCAGGA TGGAACAAGT AGTGTGAAAG 11251 AGGACTGATA CCTTGGCCTC ACACACAGTA CTGCTCTTAG ACTGGGGCAA 11301 GTGAAACTCC TCACTTCAGA GTGCCCCATT CTAGGCCCCC TCACTCCCAA 11351 AGGGGTGAGG GATCACTGGG GCCATGGGAA TGTGCTTGTT CAGCTCTCGT 11401 GGGCTCTCCT TCTGTACCAC GTTCTGGACA TCTGGAGTTC CTTGCCCCAA 11451 ATCCCTGAGC CCACGTCTGC GTCCGCACAG TCTATTTCCT AAGGTCAGTC 11501 CATCTCCTCC AGGTGGGAAC GTGCCACCAT TGACTGTGCC CTTGGGCCTG 11551 AGTGATGGCC AAGGGCTGTG TTGGGGAGTG TTGTGGATGG ATCCTGGCAC 11601 CGAGGGCTGG GATATCCTCT CAAATGAATG TGAGGTGCCT CCCAGTGCTG 11651 GAGAGAGCGG GATTCAGGAA GCAGTGGAAG GGAAGAGCCT GGGATATGGG 11701 GATCAGCTGT CTGTGCCCTG CTGCATTCTG GAATAAAACT CTGAGGGACT 11751 AAGAATTCTA AATTCAAACC TGAATCAACC AGGTTGTTAC AAAGATAAGT 11801 TTGTCAGTGC AGGAGGATAC AATATATTT ACTTAAGTTA CTAGCTCGAT 11851 TGATCATTTT TAAATTTTTA GCTACATATA GTATGTGGGC CTCCATTTGT 11901 CCTCTTATCC CAGGCCTTGC AGAATTTAGG AATAAGCCTC AATACAGTGT 11951 TCTAACCCAG TGACTTCCGC CTCGATGTAC AGTAGATTGA ACCTGATCCT 12001 TTATACTTTA GTGATCATTA GTTGATACCA GTTCAAGTCA GGCTTTCTAG 12051 AAATCTCATT GTATGTTAGG GGTTCGATTA GAGTACAGTC ATGCATCACT 12101 TAATGAATGG CCACAGGATA CATTCTGAGA AACGCATTGA TAGATGATTT 12151 CATCATTCTG TGAACATCAT AGAGTGTACT TACACATACC AAGATGGCAT 12201 AGCTACTACA GACGTAGGCT CTGTGGTACA GGCCATTGCT CCAAGGCTGC 12251 ACATCTCTAC AGGATGGTAC TGTACTGAAT ACTGTAGGCA ATTGGAGCAC 12301 AGTGGTAAGT ATTTGTGTAT TTAAACATAG AAAAGGTATA GTAAAAACAG 12351 GGTGTTACAG TCTTAAGGGC CCACCATTGT ATTTCCAGTC TCCGTTGACT

12401	GAAACATCAT	TATACAGTAC	ATGAGCACGT	ATCTTTCTCA	CCTGGTACTA
12451	GTGGAAAGCT	AGAAGGCTTA	GAAGTCTACC	TGTAAACATA	GCTTAAGTAA
12501	TAATACAGCC	TTATTTTTAA	ATGATAATAG	CAATAATAGT	GTTCACTTAT
12551	TGAGCATTTT	ACTATGAGTT	ACTTACTAAA	TATATTTCAT	CGTTAATTTA
12601	CTCTTTGTGT	TATTTGATCT	ATAACATCGT	TTAACAGGGA	AATTACCTAG
12651	TACATAATGT	ACTGTTATCT	ACATTTTATC	TAGATGAGGA	AACTGAGGCA
12701	CAGAGAAATT	AAGTACTTTG	CCTAGGATTA	CCCGTGAAGT	TAAGTGACAG
12751	AATCAATGAA	TCTGGAAGGT	CTGGCTTCAG	ATCTCTTGTG	CTGAGTCACT
12801	CGCATACTTT		AGGTTTCTAA	TCAGAGGAAT	TTGTATCTGT
12851	ATTCCCTGCT	ACTCTTACCC	TCTATGTGGG	ATTTGGCCTT	TCTCCATTAT
12901	CCCTGTGAAC	TCGCTCTGGG	ACCTTCCTTC	TTGTACTTGG	AACCATCAGA
12951	AAGTGATCTG	AGAACATAGA	AATCTACTGT	GTTGTGAAAC	AGAATTACCT
13001	GGAAGCGGAA	AAAGCCCTCC	TGGCTCAATT	CACATGTCAC	GGCTTATGGT
13051	CGTATCCGGG	GAACATATGA	AACTGGGCAC	TGAGTGCGGA	GTCAGGAAAG
13101	CCCTGTCCAT	CCTCTGGGTT	TCTGGGGAAA	ACGTGGACCC	CTTCATTGTC
	ACTTTCTCCT	GTATATTTTT	GTTTTTACTT	TTAGAACTGT	ACAATTACGT
13201	AATAAATAAT	AAAAAGTCGT	TGGAAGGATA	GGTGAAGTTC	AGAAGTGAAA
			CTCCTTCCCA		CCTTTCCTCT
13251	GTGTTTTGGA CTAATAAATA	GGAGTCTAAG			AGCAGAGTCC
13301		GAACTGGTCT	AACCAAGGAT		
13351	AACGGAGATT	CAGGGATTCT	AATAACCTCT	TGTAGAATCA	CTGGTTTGTT
13401	TCAGCCACAA	GAAGGAATTA	CCTTTTGACA	TTGGCTTGAA	CAGCTGTTGT
13451	GCAAAGAAAA		AAGTTCTGGA	AGTACCAGAT	TGATTTTATA
13501	GGTTTTTTT		GAGGGACATG	GGGGTATTGA	CAGTTGATGT
13551	TAATCAGAAA	TCCTAAATTA	TGTGTATTCC	TGGTATGTTG	CAATCAGCCG
13601	GCCACCTGGT	TTTCCTCTGG	GCTCTTAATT	TTAGGTGTAT	TCCGAGGAAG
13651	TTTTTCTAAC		ACACAGACCA	GGTATATTGC	ATACTTTCAA
13701	TGTTTAACCA	AATCTCTTCA	CTGTTTGCAG	TATTATCTGT	AGGCTCTCAT
13751	GTTTTAAGAC	TTCCCCATGG	TGTTTTTGTA	TTGTATTTTG	CTAACCTATA
13801	AACAATTCTT		ACAAGATATT	TGGGCAGTAA	CAATAAATTT
13851	TAAAAACATC	AATTCAACTT	TTTTACATTA	GGGCTTGGAC	TATGGAAAAA
13901	GTATTGGGCA	GCATGCCTCA	TACTGAGTTG	TTTAATGAAT	TTAAAAGTAT
13951	AGCCNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14001	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14051	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14101	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14151	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14201	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14251	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14301	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14351	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	иииииииии	NNNNNNNNN
14401	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14451	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14501	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14551	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14601	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14651	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14701	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14751	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14801	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14851	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14901	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
14951	NNNNNNNNN	иииииииии	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15001	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15051	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	ииииииииии	NNNNNNNNN
15101	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15151	NNNNNNNNN		NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15201	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15251	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15301	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15351	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15401	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
15451	NNNNNNNNN		NNNNNNNNN		NNNNNNNNN

15501 ИМИМИНИМИ ИМИМИНИМИ ИМИМИНИМИ ИМИМИНИМИ ИМИМИНИМИ 15801 ИМИМИМИМИ ИМИМИМИМИ МИМИМИМИМИ МИМИМИМИМ ИМИМИМИМИМ 16351 ИМИМИНИМИ ИМИМИНИМИ ИМИМИНИМИ ИМИМИНИМИ ИМИМИНИМИ 16601 ИНИИНИИМ ИНИИМИНИИ ИНИИМИНИИ ИНИИМИНИИ ИНИИМИНИИМ 17501 ИНИМИНИНИ ИНИМИНИНИ ИНИМИНИНИ ИНИМИНИНИ ИНИМИНИНИ 17551 NNNNNNGGT GGAGAGTTCT GTAGATGTCT GTTAGGTCTG CTTGGTCCAG 17601 AGCTGAGTTC AAGTCCTGGA TATCCTTGTT AACCTTTTGT CTTGTTGATC 17651 TATCTAATAT TGACAGTGGG ATGTTAGACT CGCACACAT AATAATGAGA 17701 GACTTTAAGT CTTTTTCTAG GTCTCTAAGG ACTTGCTTTA TGAATCTGGG 17751 TGCTCCTGTA TTGGGTACAT ATATGTTTAA GATAGTTAGC TCTTCTTGTT 17801 GAATTGATCC CTTTACCATT ATGTAGTGGC CTTCTTTGTC TCTTTTGATC 17851 TTAGTTGGTT TAAAGTCTGT TTTATTAGAG ACTAGGATTG CATTCCCTGC 17901 TTTTTTTTT CGCTTGGTAG ATCTTCCTCC AGCTGTTTAT TTTGAGCCTA 17951 TGTGCATCTC TGCACGTGAG ACGGGTCTCC TGAATACAGC ACAGTGACGG 18001 GCCTTGACTG TTTATCCAAT TTGCCAGTCT GCGTCTTTTA ACTGGGGCAT 18051 TTAGCCCACT TATATTTAAG GTTAATATTG TTATGTTTGA ATTTGATCTG 18101 TCATTATGAT GTTTGCTGGT TATTTTGCCC ATTAATTGAT GCAGTTTCTT 18151 CCTAGCCTCG ATGGTCTTTA CAATTTGGCA TGTTTTTGCA GTGGCTGGTA 18201 CCAGTTGTTC CTTTCCATTT TTACTGCTTC CTTCAGGAGC TCTTTTAGGG 18251 CAGGCCTGGT GGTGACAAAA TCTCTGAGCA TTTGCTTGTC TGTGAAGGAT 18301 TTTATTTCTC CTTCACTTGT GAAACTTAGT TTGGCTGGTT ATGAGATTCT 18351 GGGTTGAAAA TTCTTTAAGA ATGCTGAATA TTGGCCCCCA CTCTCTTCTG 18401 GCTTGTAGGG TTTCTGCTGA GAGATCTGCT GTTAGTCTGA TGGGCTTCCC 18451 TTTGTGGGTA ACCCGACCTT TCTCTCTGGC AGCCCTTAAC ATTTTTTCCT 18501 TCATTTCAAC GTTGGTGAAT CTGACAATTA CGTATCTTGG GATTGCGCTT 18551 CTCGAGGAAT GTCTTTGTGG TGTTCTCTGT ATTTCCTGAA TTTGAATGTT

18601 GACCTGCCTT GCTAGGTTGG GGAAGTTCTC CTGGATAATA TACTGAAGAG 18651 TGTTTTGTAA CTTGGTTCCA TTCTGTCTAT CACTTTCAGG TACAACAATC 18701 ATAGCATTGG TCTTTTCACA TAGTCGCATA TTTATTGAAG CCTTTGTTCA 18751 TTTCTTTCA TTCTTTTTC TCTAATCTTG TCTTCTTGCT TTATTTCATT 18801 AATTTGATCT TCGATCACTG ATATCCTTTC TTCTGCTTGA TCGAATCGGC 18851 TATTGAAGCT TGTTTATGCT TTGTGAAATT CTTGTACTTT GGTTTTCAGC 18901 TCCATCAGGT CATTTAAGCT CTTCTCTACA CTGGTTATTC TAGTTAGCCA 18951 TTTGTCCAAC CTTTTCTCAA GGTTTTAAGT TTCCTTGCGA TGGGTCAGAA 19001 CGTGCTGCTT TAGCTTGGAG AAGTTTGTTA TTACCAACCT TCTGAAGCCT 19051 ACTTCTGTCA ACTCGTTAAA CTCATTGTCC ATCCAGTTTT GTTCCTTTGC 19101 TGGTGAGGAG TTACGTTCCT TTGGAGGAGA AGAGGCGTTC TGTTTTTGGA 19151 ATTTTCAGCC TTTCTGCTGT GGTTTCTCCC CATCTTTGTG GTTTTATCTA 19201 CCTTTGGTCT TTGATTTTGG TGACGTACAG ATGGGTTTTG GTGTGGGTGT 19251 CCTTTTTGTT GATATTGATC CTATTCCTTT GTTTGTTAGT TTTCCTTCTA 19301 ACAGAGGCCC GTCAGCTGCA GGTCTGTTGG AGTTGCTGGA GGTCCACTCT 19351 AGACCCTGTT TACCTGGGTA TCACCAGTGG AGGCTGCAGA ACAGCAAATA 19401 TCGCGGCCTG ATCCTTCCTC TGGAAGCTTC GTCCAAGAAG GACACCCACC 19451 TATATGAGGT GTCTGTCGGC CCCTACTGGG AGGTGTCTCC TCCCAGTCAG 19501 GCTACATGGG GCTCAGGGAC CCACTTGAGG AGGCAGTCTG TCCGTTACTG 19551 GAGTTCAAAT GCCGAGCTGG GAGAACCACT GCTCTTCA GAGCTGTCAG 19601 GCAGGGATGT TTAAATCTGC AGAAGCCGTC TGCTGCCTTT TGTTTAGATA 19651 TGCCCTGCCC CCAGAGATGC AATCTAGAGA GGCAGTAGGC CTTGCGGTGG 19701 GCTCCACCCA GTTCAAGCTT CCTTGCTGCT TTGTTTACAC TGTGAGCATA 19751 GAAGTGCGTA CTGAAGCCTC AGCAATGGCG GGGAGGCGCT TCCCCTCACC 19801 AAGCTCCAGC ATCCCAGCTT GATCTCAGAC TGCTTGGCTA GCAGCAAGCA 19851 AGGTTCCATG GGCATGGGAC CCCCCGAGCC AGGCACTGGA GGCAATCACC 19901 TGCTCTGCCA GTTGCGAAGA CTGGGAAAAG CACAGTATTT GGGCAGAGTA 19951 TACTGTTCCT CCAGGTACAG TCACTCACGC CTTTCCTTGG CTAGGAAAGG 20001 GAAATCCCCT GACCCCTTGC ACTTCCTGGA TGAGGTGACG TCCTGCCCTG 20051 CTTTGGCTCA CCCTCCATGG GCTGCACCCA CTGTCCAACC AGTGCCAATG 20101 AGATGAACCA GGTACCTCAG TTGGAAATGC AGAAATCACC CATCTTCTGC 20151 ATCGATCTTG CTGGGAGCTG TAGACCAGAG CTGTTCCTAC TGGGGCATCT 20201 TGGAAGCAAC TCTGGGTCTG AGTTTCTGTT TGTTGCCCTG ATGTATATCC 20251 CCAGTGCCTA GAATGATACT TGTTACATAG GAAGTGCTTG ATCCATGTTT 20301 GCACAAATGA ATCTTTCTCA TAATGAGGTT TCTCTAAACA AGCTGTTCTC 20351 CCAAAAACTT ACACCCAGCT TTATGTTGAA GCATCTCATT ATACATTGGA 20401 AAGATGAAAT GTGTAGTGAG ACTTTGAATC TTCTTTTGAA TCTAGAAACA 20451 TTAGCATTT TAGACCATTC TATTTTAATA TTTATGAAAT TTATGAAATA 20501 ATAAGAAACA TGAGGCCGGG CTCAGTGGCT TATGCCTGTA ATCCCAGCAG 20551 TTTGGGAGGC CAGGGCTAGT GGATCATGAG GTCAGGAATT TGAGACCAGC 20601 TTGGCCAACA TGGTGAAACC CCACTTCTAC TAAAAATATA AAAATTAGCT 20651 GGGCGTGGTG GTGCATGCCT GTAATGCCAG CTCCTGGAGA GGCTGAGGCA 20701 GGAGAATCAT TTGAACCTGG GAGGCGGAGT TTGCAGTGAG CTGAGATCGT 20751 GCCATTGCAC TCCAGCCTGG GCAACATTGC GAGACTCCAT CTCAAAAACA 20801 AAAACAÀAAA CAAAAAAAAT GTGTGACCTA AATTAGGCTT ATAGATGAAC 20851 CATTGCAGTC ATGATTAATT CCGCCATTGT TTGCCTTGTG ATCTTTGGTG 20901 CCATGTCTGT ACATATTTCA TGATTTCTGT GTTTTTACGG TTTCCATTTC 20951 AGATCTCCCT TGAGTTTAGA AATCTGGCTG AGAAATACCA AACAGTGATT 21001 GCCGACATTT GCCGGAGAAT GGGCATTGGG ATGGCAGAGT TTTTGGATAA 21051 GCATGTGACC TCTGAACAGG AGTGGGACAA GGTTAGTCTC ATAAAACAGT 21101 GTCTGTGTT GATGTATTAG ACAGAGCTGG CAGTCCTCAT AGTGAAGCTC 21151 AGAACAAGAA AAGTTGTCCA GTATTTTCAG CCCCTCTGGT TTTACAATTC 21201 ATCTGTTTAG GTTGAATGTC TCATCATAAA CAGTTTATTC CAGAGTTAAT 21251 TCCAAACCAG CAGCTATGTA GGATATCAGC CAGGCTAGGA GTAGGGTACT 21301 GGAGAGAGT GCTTATCTAG ACAAAGGGAT GTAATTGACC ATGAAGATTA 21351 AAACTACACA TCAAAACATA AGGTAGGGTT AGGAGTCTTG CCTATTTTTC 21401 ATAGGAATGG TGTTTGTGAG ACTTACTCAT CACTTCTGTG GAAGTAAAGA 21451 CATTTTATTT ATTTATTTA AAGCCAGTCA GATTTAGCAG GCAGAGACAT 21501 TTCAGACATC TAAAGTGTTG ATGTATTTCA TACCTTTAAC TGTGCTTAAA 21551 TTAGGATCTC CGAAAAGATG CTGCTACATG GTCACTACGT TAGTGTAGGT 21601 CCAAGGTCTT GGGCCTCTTA ATTTTTCAAA CCTCAAAACT TGACAGCAGT 21651 TATCTTTGGA ACTGCTGATT TGTGCTTCCT AAGTTAACAG CATACAATGA

21701 CTGCTAGAAA TCAATTTCTG CATTTAAGGT GAAGTTAGCC GGGTACTATG 21751 GTTTACCTGT AATCTCAGCA CTTTGGGAGG CTGAGGTGGG AGGATCATTT 21801 GAGCCCAGGA GTTAGACACA AGCCTAAGCA ACATAGCGAG ACCCCGTCTT 21851 TCAAAAAATT AAAAAATGAG CAGGGAATTG GTGGCATGTG CCTGTGGTCC 21901 CCAGCTACTC TGGAGGCTGA GGTGTGGGAG GATTGCTTGA GCCCAAGAGT 21951 TGAAGGTTGC AGTGAGCCAT GATTGTGCCA CTGCACTCCA ACGTGGGTGA 22001 CAGAGCAAGA CACCTACTGA AAGAAAATAA AGTTGAAGTT AAAACTTCTG 22051 GCCAAGAACC AGCACTGGTT ATGATAGTAA CTCATTTTCT GTTGTGCAGA 22101 TTTATTCAGG AAACTTAATT TTAGGTTGTT GAATAGAAGT TTTGATCAGA 22151 TAAAATTGAA TTAAAAAAAA TTTTTTTTGA GACAGGGTCT TGCTGTTATC 22201 CAGGCTGGTG TGTAGTGGTG TGATCACGGC TCCCCGCAGC CTCAACCTCC 22251 TGGGCTCAGG TGATCCTCCC ACCTCAGCCT ACCGAGTAGC TGTAACTACA 22301 GTGCATGACA CCATACCAGG CTCATTTTTG TACATTTTTT GTAGAGAGAG 22351 GGTTTTGCCA TGTTGCCCAG GCTAGTCTCA AACTCCTGGC ATCAAACAGT 22401 CCTCCCACTC TGGCCTCTCA AATGTTGGGA TTACAGGCAT GACCAGCCAA 22451 TTATTTCAAG GAGTTATTTT TTTTCTTCTA CTTTGGGGGA AGATGAATTA 22501 TATAAGTCTC CATTTTAGGA GTATTTCTAC CAAAAGAACT ATTATCTTCA 22551 AATATATTT TGGATAGTAC TATAGATATA CTAATTTTT TTTAAATTTC 22601 TAGTAATTCT TTTGAAGATT TTGTATAGCT GTCCAAAGCC AATTTCTGTC 22651 TACCTAATTT CAGCAAGATT TCACTCTTTT CATGTTACTT TTGTCCCAGA 22701 ACAAATTTCA AGTGCTTTCT CTTCACCTGT GCATTCTTCC CCCTGATTAG 22751 TCTCTGGCTT TGTATTACTT TCAGTCAGAG ACGACTTTTT TTTTTTGAGA 22801 CAGGGTCTCA CTCTGTCACC CAGACTGGAA TGCAGTGGCA CAGACAAGGC 22851 AGCCTTGACC TTCTGGGCTC AAGCAATCTT CCTTGCCCTC AGCCTCCTGA 22901 GTAACTGGGA CCACAGGCAC GTTGCCACCA TGCCTGGCTA ATTTATTTTA 22951 ATTTTTATTA TTTTTGAGAC AGGGTATTGC TCTGTCACCC AGGCTGGAGT 23001 GTAGTGGCAT GATCAAGGCT CACTGCAGCC TTCACCTCCT GTGCTCAAGC 23051 AGTCCTCTCA CCTCAGCCTC CCCATTAGCT GGGACTATAG GTCCACCACCA 23101 CTACACCAGG CTAATTTTTG TAATTTTTTG GTAGAGACAG GGTTTCATCG 23151 TGTTGCCTAG GCTGGTCTTG AGCTCCTGGG CTCAAGCGAT TCACCTGCCT 23201 TAGCCTCCCA GGTGTGAGCC ACTACACTCA GCCTTTTAAA ATTTTTTACA 23251 GAGATGAGGT CTTGCTTTGT TGGCCAGGCT GGTCTAAAAC TCTTGGGCTC 23301 AAGCAGTCCC CTCTCCACAG CCTCCCAAAA TTCCGGGATT ACAGGCGTGA 23351 ACTTCGGTCA TTTCCTAACT TTTACCCTTC CTAATGACAC TCCAGAGCTT 23401 ACCTTCTTTA CTTTTGCTTC TTAAGTTAAC TAATAGACAA TTATTGTATG 23451 TGGATATTGC ATTAAGTTGT CTTAGGATAC CCTTTTCAGA GGAGGACAGC 23501 TTTTGACAAA TTGCTGTCGC GGAAAAAAA AGTATTTGGC AATTAAGAGT 23551 TGCATTTACT GAAATCTCTG TTGAGAGAGG GGAAGTTACG TTGTCTCTAA 23601 AAGAAAAACT AAAAAGAAAA GGGGAAGTTT TAGCAAAGTT GTTAAAGCCT 23651 GACACTTAAG TCATACTACC TAGTTTTGAA CTCTTAGCCC CTGCCACAGA 23701 CACGGCAGCC CCTTGAACCT TCCTGGGTTC AAGCGAGCCT CCTACTTCAG 23751 CCCCCTGAGT AACTGGGACC ACTGGCCTGT GTCACTGTGC CTGGCTAATT 23801 TTTTTTTTT CCTCACATGG GCAATGTTGG GCAAGTTAAA TCGACTTCTT 23851 TGTGCCTCAG TTTCCTCATC TGAAATGGAG ATCATACTGC TATGTACCTG 23901 ATACAATGTT TGTGAGGATT GAATGTGCAG AGTTCTTTTT TTCTGTTGTT 23951 GTTGTTTTGA GACGGAGTCT CACTCTGNNN NNNNNNNNN NNNNNNNNNNN 24101 CGCCCGTCTC AGCTTCCCAA AGTGCTGGGA TTACAGGCAT GAGCCATCGT 24151 GCCCGGCTGA ATGTGCAGAG TTCTTAAAAC CGTGTCAAGA ACATAAAATA 24201 GTTATTTGTT CTTTCATATA ATGATGATTT TGAGGGCCTG CGGATCTTGA 24251 CATGTTATCA GATTGGTCAA AAAAAGATTA AACCATAGTT GGTATTGTCC 24301 TAGTTCCTGT TACCAGAATA TTCCATCTTT CATCGTTGCC TTCTCTCATA 24351 GTTTTATGTA TCAAAAAGTT TATTGTAAAG CTAGGCCGGG CACGGTGTCT 24401 TGGGCTGGTA ATCCCAGCAC TTTGGGAGGC CAAGGCTGGC AGATCAGTTG 24451 AGGTCAGGAG TTCGAGACCA GCGTGGCCAA CATGGTGAAA CCCCGTCTCT 24501 ACTAAAAATA AAAAATTAGC TGGATGTGGT GGTGGGTGCT TTAATTCCAG 24551 CTACTCAGGA AGCTGAGGCA GGAGAATCAC TTGAACCCAA GAGGCAGAGG 24601 TTGCAGTGAG TTGAGATTGT GCCACTGCAC TCCAGCCCAG GGGACAAAGT 24651 GAGACTTGAT CTCAAAAAAA AAAAAAAAA AAAGTTATTG TAAAGCTAGA 24701 CACGGTGGTA TTTGCCTACA ATCCCAGCTG TTCGGGAAGC TGAGGCAGAA 24751 AGATTGCTTG GGTCCAGTAG TTTGAGTCTA ACGTGGGCAA ATATATGAGA

24801 CTCCATCTCA AAAAAAAAA TAAAAAATAA AAATAAAAA ATGTTTACTA 24851 GTTTTTTCA GTAGCCTTTT ATTATAGTAG CAGTACATGT GTATTGTAGA 24901 AATTTGGAAA ATACAAGTGA AAAATAAAAA CATCAAATTC CCGTCAGCCA 24951 GAGACTGCTG TGAAATGTTT TGAGCACATC CTTCTTGAAT GTTTTTTAAA 25001 TCCTGGTATG TATATTTGTA TTTTAAAATC AAAATGCATT CTTACCCATT 25051 CTCTTTTGAA CCTGCTTTTT TGTAGCTAAT GATCTCTAGT GTGTCCATTT 25101 CAGTAAAAAT TCCATTATTA AAGTGCTTTA AAAATCGTCT CTTACAGTAC 25151 TGCCACTATG TTGCTGGGCT GGTCGGAATT GGCCTTTCCC GTCTTTTCTC 25201 AGCCTCAGAG TTTGAAGACC CCTTAGTTGG TGAAGATACA GAACGTGCCA 25251 ACTCTATGGG CCTGTTTCTG CAGAAAACAA ACATCATCCG TGACTATCTG 25301 GAAGACCAGC AAGGAGGAAG AGAGTTCTGG CCTCAAGAGG TAACAGATTC 25351 AGGGTATTTT GGGGGAAAAT AACTTTAGAC ATTCTCTGAA AAATCCTTTA 25401 ACTCTTGTGG TTGCGGGTGA CAGAAAAACA AGCCAGGCCT CCCCCAGGCA 25451 GCATAAGGGG ATGTGGAAAA TAGGATAGAT TGACATGAGT TTGCTTCAGG 25501 TAGACTGGCT GACTCCCAGG ATTCACACCA CGTAATCAGT ATATTCAAGC 25551 CTTGCTGTCC TTGATTTCTT TCAGACGGTC TTTCTCCAAG TGGTGGATAT 25601 GGTAACAACC CACGTGCACT AGCTTAACAA AAAGTTCTTA GGAATGGCTT 25651 TGTTCGGCCT GGCGCAGTGG CTCATGCCTG TAATCCCAAC AGTTTGAGAG 25701 GCCAAGGTGG GCGGATCACC TGAGGCCAGG AGTTCGAGAC CAGCCTGGCC 25751 AACATAGTGA AACCCCGTGT TTACTAAAAA ATACAAAAAT TAGCCGGGCG 25801 TGGTGGCAAG GGCTTGTAAT CCCAGCTACC TGGGAGGCTG AGGCAGGAGA 25851 ATCGCTTGAA CCCAGGAAGC AGAGATTGCG GTGAGCTCAG ATTGTGCCAC 25901 TGCACTCCAG CCTGGGCGAC AGAGTGAGAC TCCCTCTCAA AAGAAGAGGA 25951 AGGGCTTGGT TCTTCTGCTC AGCCCTGAAT CAGTTACTGT TGCTACACAG 26001 CTGAGTTCTC TGGCCTCACC TGGATTACGT CTACACAGTA CACACAGAAT .. 26051 GGATTTCCCC CAAAGAAAGA ATTCTGCGGC AGGAAGGGGA .AAGGGATGGC 26101 AGGTAGACAA AAACTCCAGG TGTCTGTAAT AAGGGACAGG GTCGATCTTT 26151 AATTAAAACA TGGACAGGGA ACAGAAAGCT TTTGATACTG ATTTTGTTCA 26201 GAAGGAAAGT AGAAAATTTT ATGACTGTTC CCTGAATTTA TTCCAGCATT 26251 TACCTTTTGC TTTCCATAAA AGTGTTTCCT GCAGCCAAGT ACTTTAAAGT 26301 TTTAAAAAGA CGGGTGAGGC TAAGTGTGGT GTCTCATACT TATAATCCCA 26351 GTGCTGAGGC CAGGAGTTCA AGACCAGCCT GAGCAACACA GCAAGATACC 26401 ATCTCTATAA AAAATTGTTA GAAAATGATT CTGCTGAAAG AGCAAAAATA 26451 AAAATTAAAG AAAGTAGAAA AAATAAAACT AAATTTAAAA GATTAACTGG 26501 GCATGTTGGC ATGCACCTGT ATTCCTAGGT ATTCGGGAGG CTAAGGCACA 26551 AGGATCCCTT GAGCGCAGGA GCTCAAGGTT GGATTGAGTT GTAATCACAC 26601 CACTGCACTC CAGCCTCGGT GGCACAATGA AACTGTCTCA AGAAAAAAAA 26651 AAAGTGACAG AGGGAAACAA TATTTGCAAT TCATAGAGCA GATACAGGGT 26701 TCATATTCCT AATATTAAAA AAAACTTCTA AAAGTTAAGA AAAAGGCCAA 26751 CTGCCCCACA GAAAAATGGG CAAGGAGATA AGAACAAGAT TGTTCACAGG 26801 AAGAGACACA CAGATGATTA TTAAAAATCT GAAAAGATGC TGAGTCTTAC 26851 TCCTAAGAAA AATTCACATT TAAACTACTC TGGGGGCTGG GCAAGGTGGC 26901 TCACGCCTGT AATCTCAACA CTGGGAGACC AAGGCAGGAA GATCACTGAA 26951 GCCAGGGTAT CGAGACCAGC CTGGACAACG TAGTGAGACC TTATCTCTTA 27001 AAACAAAACA AAACAAAACA AAACAAAAAA AACAGTAAAA ATTGGCCGGG 27051 CACAGTGACT CCTGCCTATA ATCCCAGCAC TTTGGGAAGC CCAGGTGAGT 27101 GGATCACTTG AGGTCAGGTG TTTGAGAACA GCCTGGCCAA CATGGCAAAA 27151 TTCCGTCTCT ACTAAAATTA CAAAAATTAG CCAAGTGTGG TGGCATACGC 27201 TGGTAGGCC AGCTACTTGG GAGGCTGATG TGAGACTCCA TTTAAAAAAA 27251 AAAAATCAAA AATTAGCTGG GTATAGTGGC ACACCCCTAT AGTTCTCGCT 27301 CCTTGGGAGG TTGAGGCAGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT 27351 GCAGTGAACC ATGATCACAC CACTGCATTC TAGCAGCCTG GGAGACAGAG 27401 CAAAACCCTT GTCTCAAAAC AAACAAACAA CAACAAAAAC AAAAAACACT 27451 TCCCTCAGCT CAGACATGGC CTTTTAAGTT TCCTAGGTGA CTCGTGTGCA 27501 GCCAGGGTTG AGAAACCACT CTTGTCTTAC CCCTCTTTTG CAGACACAGG 27551 GCTCAGAGAA GGGAAGGGGA TTGTCTGGGG ATGTATAGTG AGGCAGTGGC 27601 TGCCTTGGAA GTGGAGTCTC AGTCTCCCGG CTCCTAGGCC AGCCCCTGAC 27651 CACTGTTCCA TTGTCTCCCA GACAGAACAT CAGCCACGGG CATGTGATGC 27701 ATGAGCGTGA GCCACACCAT CTTGCACACA CAGGAGCAGA GCCCTGCTCT 27751 TCTCATTCAC TTACTTTATC TGTAAAATAG CATCATTTCT ACCACACGGT 27801 GGTGGTGTGA ATAAAATGAG ATGAACTTCT AGCATAGAGT GCTTAGTAAA 27851 GGTTCTGGAC ATTTCGTAGT AGTTGAATCA TGCCAAATGT GGTCCTAGGT

27901 GATTGGCTTC TTTTGCTAGC ATGTTTTCAG GGCTCCTCCA TGCTGGGGCA 27951 TTGCATCACT GCTTTATTCC TTTTTATCGC CTAGTATTAT TCCACTGTGT 28001 GGATAGACCA CATTTATCCA TTCATCAGTT GGAGGATATT TGGGTTCTTC 28051 CCATTTTTT TGGCTATGGT GAATAGTACT GTGTACATTT GCATATAAGG 28101 TTTTGTGTAG ATGTGTGTTT TCCTTTTTCT TGGGTCTATG CTGAGAAGTG 28151 GAATTGCTGG TTCATACAGC AGCTCGAACC TTGTGAGGAG CTGCCAGACG 28201 CTTTTCCAAG GTCGCTCCAC CATTTTACAT TCCCGTCAGC AGTGTGAGAG 28251 TCCCAGTTTC ACCAGCACTT GTTGTTATCT CTTTTTAACT GTATGTATAT 28301 ATACTTAACA TTTTATTTAT AATAAATGTA CATAATAGAG AATTTGCCAT 28351 TTTAACTATT TTTAAGTCTA TTATTCAGTG GCATTAAGTA CATTAATGAT 28401 GTTATATAAC CATCAACACT ATGTTTCCAG AACTTTCGCT AGCTTCAGAG 28451 AATCCTCTAA ATAATATCAT TAAAAATCAT CAAGCCGAAT CCCACTGTTA 28501 GAATTAAAGG TTTTATTTCA CTTTCAAGTT ATCAGGATCC AGGGAGGTGT 28551 AATACACTTA GAGGATAGAC TCAGCTCATT TCCCAGCTAT GCCTTTCAGC 28601 AGCATTCTTA CCAGAGTAGG AATATAATGT TAGTCATTAT TTAGAGGCCT 28651 GGCCATCTTG AGAAGGTTTA CTGTTTAGTC TGCAGTACAA TTATAACTGT 28701 TTTTGTATAT TGGGTTATTT TTTTCAGAAG TAGGCCAGTA GCTCTAACAG 28751 GAGCCTCTTT AGCCTGAATT CGTCCAAGTA GTGCAGTGTT GCACTAGTTG 28801 TCCCTCGGGA CÀTGCTCCCC AATACGTAAC TCACTTCCAG GTTGCAACTG 28851 GACACTTACT GGTAGTCAGA AATAGCTATT GCATGGAGCT TAAAATGAAC 28901 TTGATCTTCG TGAAAGATGA GTCTGCAGCT AAGAGACTTT ACTGTATATC 28951 ATAGTGTTTT TTTTTGTTTT GTTTTGTTTT TGTTTTTGTG ACGGAGTCTC 29001 ACTCTTTCAC CCAGGCTGGA GTGCAATGGC GAGATCTTGA CTCACTGCAA 29051 CCTCCGCCC CTAGGTTCAA GCAATTCTTC TGTCTCACCC TCCTGAGTAG 29101 CTGGGATTAC AGGCGCCTGC CACCGTACCC GGCTAGTTTT TGTATTTTTA 29151 GTAGACACAG GGTTTCACCA CCTTGGCCAG GCTGGTCTTG AACTCCTGAC 29201 CTCGTGATCC ACCCTCCTCG GCCTCCCAAA GTGCTGGGAT TACAGGCGTG 29251 AGCCACGGCG CCCAGCCTGT ATCATAGTTC TTATGCACAA AGACCCTTTA 29301 ATATTGTTTG TAAATTCTCC CCTATGCACA CGCTGACCTG TTCCTTAATC 29351 TTCTTATCTG TCTAGGTTTG GAGCAGGTAT GTTAAGAAGT TAGGGGATTT 29401 TGCTAAGCCG GAGAATATTG ACTTGGCCGT GCAGTGCCTG AATGAACTTA 29451 TAACCAATGC ACTGCACCAC ATCCCAGATG TCATCACCTA CCTTTCGAGA 29501 CTCAGAAACC AGAGTGTGTT TAACTTCTGT GCTATTCCAC AGGTAGGGAA 29551 CGGGGCTCCT CTGGGTGGAT ACGGGGCTAA AGGGAGTGGG GTAGGAGTAA 29601 GGGTGGATTT TGCTGTGCTA TATTCAAGGA TATGATTCCT TAAAAAGACG 29651 ATGACTCCAG TTTATTACGC TGGGAGTTTC ATAGCACCCG CCTTTGCTTC 29701 CAGCCACCAA ACTCAGCTCA GCCTTGAGGT TAAGCCTGCT CCTTTTCAGA 29751 ACCTTCTTC CGGATTTACT ATTTTCTACA GCTATCCTAA ACTAGTTAGG 29801 TTCTTTCCT CACAGTTAAG TCAAGGTCTT TGGCTTAGAT TTATGGGGAG 29851 TGCTGGGTAA AACCTGGGTG AAGCTGTTAT CATTAAAAAG TCTTCATTAA 29901 GCACCTAATT ACTGCTGTCC TTTTCCTAGA CCCGGCATAA AAAGAACCTG 29951 GTCCGGTAGA CCTAGCCTCT CAGTATGCTA GGAACTTACA CTTTTTAGTT 30001 GCCTTTACCA AGTATTGCAG ATACTACTGC AAATAAGTGA AGAAAGTAAC - 30051 AGCATTTAAC TGATTTGGGA ACTTGGTTTG ATCTTGTTCT AATGACCCAC 30101 TTCGAATGGT GGTTGAAAGT AAAATCTGTA TCGCCGTCTT ATGTTTCCAT 30151 TTACCTAGAA ATACTTTACC TTTGAGCACA GGAAATTAAT CCCCTTCTGG 30201 TTGTTCTCCC CCTGGCATTG GTTTTAAATA TATAATGATT ATGTTTGTTG 30251 TAGGAAAAAT AGAAAAACAA CTACAATAGA AAATTCTTCC CATATATTAT 30301 TTTGAAATAC ATATTTCCGA TCCGATAATC CATTGCTCTA GCATGGAAAA 30351 TGTTGGATTT ACTTGTGTTT GCTTTTTCCA AATAAAATGG AACTTTTGTG 30401 GCTACATTAT AGAATTGTTT TAGACTGCTT AATTCTGTGT GTTGTTGAGA 30451 AAGGGAGGAG TGGGGAAGGT AAAAATCTTG ACATACTTTC TTCGTGGGTA 30501 TTTTTCTTG AGCGATTCCA TCTTAGTTGA TTAGCAGTTA GCAATTGCCC 30551 ATTCAACAGA AGGTTTTCTT ACCTTTTTGT GATAATGATA GCTAACGACA 30601 TCATTTCTTC TTTTTTCCCT CTCTTCTTGT TGTCTCTAGG TGATGGCCAT 30651 TGCCACTTTG GCTGCCTGTT ATAATAACCA GCAGGTGTTC AAAGGGGCAG 30701 TGAAGATTCG GAAAGGGCAA GCAGTGACCC TGATGATGGA TGCCACCAAT 30751 ATGCCAGCTG TCAAAGCCAT CATATATCAG TATATGGAAG AGGTGGGTTT 30801 TTATTTAACT ACTTGGATAA TTTGTAGCTA CTTTTATGAT TTAGTAATGT 30851 CACTGTTTAA CCAGGTTTGG ATATTAGATG ATCCTAACAA TTCACTATCC 30901 TGTGGCCTAA AGAGACAGGA ATTGATATCC TTTATAAGGA AAAAAGTCTA 30951 TTCACAGGAG CCGAGCAGAT TGCTCACTGC TGTGTAGTAC CCTGGTGAGA

31001 GGAGATAAAT GGAGCAAGGC TGTAGGTTGG AGCCCCTCAG TAGAATCATA 31051 GATTTTGAGC TGCAAGATGA TGCAGGAGGC CAACCAAGCT TCTTGTTGCT 31101 GGTGAGGAAT GTGAGGTTGA AGCTTGTCTG TGCTGATGCA GTGCGTGATT 31151 GAGTGGATCT CTGGCTCCCG TCCATGTGTC CTGACACCCA GTCTGGTACT 31201 TTCATTATGC CACAGGCCTC AATTGAAAAA TCACAGTAGG GAATTTAGGC 31251 CAAGGAAAGC CATCAAGTTG CAATTATTTC CTAAATTTTC TTTGGAAAAT 31301 TTCATTTCAA ATACCAAAAC CATCCTATAA AAAGAAAACT TACCTTCTTA 31351 GGTCAAATCT CTAATATTTG ACTAGGTTCA AAAAGTTTAT TTCTGGCCAG 31401 GCACAGTAGC TTACTCCTGA AATCCCAGCA CTTTGGGAGA CCAAGGTGGG 31451 AGGATCACTT GAGGCCAGGA ATTCAAGACC AGCCCGGGCG ACATAGCAAG 31501 ACCCCATTTC TACAAAAAT TTAAAAATTG TCATGGTGGT GCACGCCTGT 31551 GGTCCCAGCT ACTCAGGAGG CTGAGGCAGG TGGATCACAT GAGCCTGAGA 31601 GGTCGAGGCT ACAGTAAGCT GTGTGATTTC ATCATTGCAC TCTAGCCTGG 31651 GTGATAGAGT GAGACTTTGT CTCAAAAAAA AAAAAAAAA AAAAAGTCTT 31701 AGAGACCAGA AGTCTCTGTA ATCTCTAATA ATCTCTAGGC CCTAGAGCAG 31751 TGGTTTGTAA ATGGAGGTGA TTTGCTCCCC TCCCCCAGA GGACATTGGA 31801 CAATGTCTGG AGACATTTTT GATTGTCCTA ACCGGCAGGA ATCGGGTGCT 31851 ACTGGCATCT GGTGAGTAGA GGCCCAGGAT GATGCTGTGA TCCTCAGGTG 31901 TGATCCTGTT GAGAATGAAA CACTGTAGAC TTTATGAAAA CATACAAGAC 31951 CCTCATCATT TTTCCTTTGC CTGAGCTCCC TCCCCAGAGG TTACCTCTGT 32001 TCATGGTTTT GTGCATCCGT CTAGTCCCCC TGTTACGCGT TTACAGGAAT 32051 ATGGTTTGCA ACAGTGTTTT CATCTAAATA GAATTATACA AAATAGCGAT 32101 TTCTGATTTC TCTTGCATAT TGCACATTCT TCTTATACTT CCTCCCTACC 32151 TTTATCTGAC ACAGAAATGC TGTATGTCCA GAACTTCTAT CAGAGGCACC 32201 TATGGAAGTC TAAGGGAAGA CCACATCGCT TTTAAAAACC CTAAAATTTT 32251. GTAGTCACTA GATGAAAATA TTCAGCCAGT GACCCAAAAA ATTGCTACCA 32301 ATGAGACTCT CCATTTTGCC ATGTAGCCAG AACTTACTTT GATCTATGTG 32351 CCTGGGGTAG TGACCAAGTA GGTGGGTAGG AGTAATCTCA GGGAAACTTG 32401 AGGCCCCAGC CTCATGGCTA GGGTCATAAT TTGAACCCAG GTCTGTCTGA 32451 CATCAGAATC CATGATGTTA ACCCCAATTC TAAGGGGTTC AACTACCCTT 32501 TCTAAATGGA ATCCTGCTAT ATTAAGCACT ATTTATTCAT TTTATATAAA 32551 CTAGAAACAT TTTATGTAGT AAGTAGTTGA GAGTGTTTTG GTTTTGCAGT 32601 TTGATCACTA GTTTTAGAAA CCAGTTTTTA AACACTTTGT GGCCAATTCC 32651 ATTACTATAT TAAAATTCAG ATTTATTTGG TTTTTCCTTA ACTATTGGGA 32701 TTAAATCCTG GTTGTAATTC ATAGTTTGAG GGCGAGGGTG GGCAGTCTAC 32751 ATTTGGCTGA GCCCTGTTTT TGTGAATAAA TGTTATCAGA ACACAGCCAC 32801 ACCCATTTGC TTCTATGTCT TCTGTGGCTG CTTTTGCAAT GTGACGGCCG 32851 AGTTGAGGAG CTGCAACAGG CGATGACTTG TAAAGCTGAA AATATTTTTT 32901 GGCCCTTGAA TAAGAGGTTG GCTGACTTCT GACTTAGGGC ATCAGTTGTT 32951 CTGTTATCCC AGTAAAACTC AAGGCATTAG GGGAGAAATG TTAATATTAA 33001 TACTTAAGTT GATTTGATTT AGGGAAATCT TTGAAGATTT CTAAGTCTTA 33051 AGCAGTAGAA CCTGTTAATG GTTTTAGTTT CAGCAGTAAG GACATTTTAC 33101 AAGTAAAGTT TTAAATGAAA ACATTTTGTA TGAAGCCACA AGTCGTCTGG 33151 CCTCTTGCTG GTGTCCAGAT ATTAACACTG ATCCTATTTC TCCTTGCTGA 33201 CCAAGTCTGT CCTTTGTAGT AAGAAAGGAA GAAACGTTGA CTCTGTCCGA 33251 TCTCTGGACT TAGTGTTGTA GCGAGCATGC ACCTGGAAGG GACTTGCCAG 33301 AGGACCTCCT CATGCTTCTC CAGTGCTTAG TGGGGGCTTG GAGTGCAGCC 33351 CCAGGTCTTC ACGAGCAGTT GGCCACACTG CAGGGCCCTC ACCCCACTCT 33401 GGAGCAGCCT CTGCTTCAAA CCAGCCTGGA TGCTTGTCAG CTGGGGAGAA 33451 GATCAACCTG CTATTTTGGG ATAGAAATAA ATGCTCAGCC AAACGGCCAG 33501 AAACCCCCAT TCCCCTCTCT GCCAAAGTGA ATTCCTTGGC AGGGAGAAGC 33551 TTGTTCGTGT CTCTGCACAC TTCCTGTGCC CTCCTGTGGT TAAGTCAGAG 33601 AATCATCCGG CTCTTTGAGC CCCAGGTGCC TAGCTGCTCA AGGATGGTCC 33651 CCAGCCAGCA GCTGCCAGGA ATCACCTGGG AGCCCATTAA GACATCCAGC 33701 CCCCACCCAA ACCTATCGAA TCAGAATCTG CCTTTTTTTC CCAAATGATG 33751 TTTTTGCTTT AATGGAAGTT TAGATGTTCA TAGACAAGAG TTTTAAATGA 33801 TGATCAAGCT GATTCCATAT TCGCAGTTGT AAGTAGAACT GCTGAGACGT 33851 GGAAGTACCA CATGGACTCA CAGAGGAGCT GCTGTATGTA GCACAGCATT 33901 GCACAAGAGC TTATTTCAGT CTAGTAAACA TTTATAGGAG CCTGTGTCAT 33951 TTAATCATCA AGCCTCGCAC TGTGGCTCAC ACCTGTAATC CCAAAACTTT 34001 GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TAAGGAGTTC GAGACCAGCC 34051 TGGCCAATAT GGCAAAACCC TGTCTCTACT AAAAATACAA CATTTAGCCA

34101 GGTGTGGTGG TGCACACTTG TCATCCCAGC TATTCCGGAG CCTGAGACAT 34151 GAGCATCGCT TGAACTCGGG AGGTGGAGGT TGTAGTGAGC TGAGATGGCA 34201 CCACTGCACT CCAGCCTGGG CAACAGGGTG AAGGCCCTTT CTCAAACTCC 34251 TCAAGTATTT GGCTTCAACT TTATGCCGGG CATGTAGATG AAAAGTCGGC 34301 TATGACCTGT CCTTGACAAG CAGATGTAAC TCCTTGATTG AGGCTAGTAG 34351 GTTTTTAAGA CCTGAATAAT TGAGTTTGCA GAAACCTACT GTGTGCCTTC 34401 AGGTAAATGG AGAGTGGGGT TTGGTCTAGC AACGAAGCAT CTAGAAGGTC 34451 TCTTTGGCCT TACCGGCTCT GTTTTAGGTA AGTCCACGTC TGAGTACCAG 34501 TGACTGCAGC TCTTCCAGTT GTGCTGTCAT GTTTATATGT TAGAAATGAT 34551 CATCAAAGGA CTCAAAAGTT TTGCCACTAA TTGTATTACC GGGGACTGTC 34601 ACAACCAAGA TTTCTCTTAA TTTATTCACC TTACTTATCT CCTGGAAGGG 34651 CATATTGAAG TGCTCTTGGA GTTCTCTAAA AGGGTTTTTG TTGGTTGTGT 34701 ATATTCACTT GGGTGCCAGC GATTGATTCC AAATAAGTAA ATCTTTTTTC 34751 CCAAAAGGAT GTAAGATGGC TTATGGTTAT AAGTACAACA GGCTAACAAA 34801 GTACAAGTAG ATGAGAAAGT AAAATGAAGA AATAAAGTCA TAGGAGCCAC 34851 AGAATTAACC CAGGAATGAA TAAGTGTGTA GTTTGGTGCT GATGTTATCA 34901 TCCTTTATTT GTACATTGCT TGTACAGTTG CTCTGAGAAG GTAAGTCTTA 34951 AATTTTCAAA AGTGAAATGT CACCGAGCAT GGTGGCTGAT GCCTCTAATC 35001 TCAGCACTTT GGGAGGCTGA GGCAGGCGGA TCACTTGAGG TCAGGAGTTC 35101 AAAAAAAAA AAAAAAAAA AAAAATCCAA AAGTTAGTTG GGCATGGTGG 35151 CAGGTGCCTG TAATCCCAGC TACTTGGGAG GCTGAGGCAG GAGAATCGCA 35201 TGAACCTGGG AAGTGGAGGC TGCAGTGAGC CAAGATTGCA CCACTGCACT 35251 CTAGCCTGGG TGACAGAGCG AGACACCATC TTAAAAAAAA AAAAAAATCT 35301 ACAATATACC AAAACCATTA CTTACCTGAG AAACTATTCT CAGGGTCATT 35351 GTAGTGAATG CCTATTTTAT GGCTTTTGAT GGCATCAGGG CACTCAGGTC 35401 ATTTACAAGA GTAGTGTGTG AGACCCTGTG TGTCACTGCC ACTCATCTTG 35451 GCCTTCGGCC ACTGCTGTAG CAACCAGTTT CCAAGTAGGG CTGGACCTTG 35501 CCTTCTGCTC CAGAGACCTC TCGCTTCCTG CCCTTGGGCT TCTGACGAGC 35551 TGCAGGAACT GCCTGGCACG TGGGTCCCCA CAACCCAGAG GAGGTGAGGG 35601 CCACCTCTCT GCTCCTCAGG GCCACCTTTC ATAAGGCTCC TTGAAGGTCC 35651 CTCAAGATCA AGCCAACTCA ACACATCCTT GATAGGCCTT CCTGCCTTCT 35701 GTTTCACTTC TCCACTCGTT TCCAAATAAA TGGCTGCATG CAAGCTTTTG 35751 CCTCAGGTTC TGCTTTTAGG AGGAAGGCTA AGACAAGCAG TAAAGCAACA 35801 TGGGCAGGCA GAAGGATGAC TTCTAATAGA ATTATCTCAT CACTATATAT 35851 TTTACTTTAT GGATGCTTGT ATTGAAAAGT CTTGGCTGGG TGGAGTGGCT 35901 CACGCCTGTA ATCCCAGCCC TTTGGGAGGC CGAGGTGGGT GGATCACTTG 35951 AGGTCTGGAG TTTGAGACCA GCCTGACCAA CACTGGTAAA ACCTTGTCTC 36001 TATTAAAAAT GCAAAAATTA GCCAGGGATG CACGCTTGCT GTGTGCCAGC 36051 ACAGGGCTAG GCTGGAGATA AAAAGGTGAG TAAGTAGGTG CGGTGTAGTC 36101 AGGGTGAAAA CTACAGATGG TCCATTTCCA CGTAAGTGGA AAGGTAAAGG 36151 TATGTACAAT AGGGTGGCTC CTGGCTGAAC CTGGAGCTGC AGACAGGTTT 36201 TCTAGAAGGC ATAATCCTGA AGTTGAGACT TGGGGGCCTA GGTAGGAGCC 36251 AGTTGAAGGG ACGTGGGAGG CGCATTCCAG AGAGAAGGAG TGGTATGAGA 36301 CTGGAACAGA GGTGTGCAGC AGCATCGCAT GGGCGAAACA ACAGTAGACA 36351 GTTGTTCTTT TGTTTTTGTT TGTTTTTTGA GACAGGGTCT TGTTCTGTCA 36401 TCCAGGCTGG AGTGCAGTGG CATGATCTCG GATCACTGCA ACCTCCACCT 36451 CCCAGGCTCA AGTGATCTTC CCACCCCAGT CCCCAAGTAG CTGGGGGACC 36501 ACAGGTGCAT GCCACGATGC CCGGCTAATT TTTGTACATT TTGTAGAAAC 36551 AGGGTTTTAC TGTGTTGTCC AGGCTGGTCT TAAACGCCTG AGCTTAAGCA 36601 GTCTACATGC CTCAGCCTCC TGAAGTGCTG GGATTCCAAA CATGAGCCAC 36651 TGTGCCTGGC CCGGCAACTG TTACTAGACT ATAGAGAGGG AGGTGGGCAA 36701 GGGCTGGTGA CACTAGACAG GTGCAGTAGG TCTGGACCAT GGGTGGCCTT 36751 GCGCTACACA TTACAGAGCT CAGGCTTTTT TTCTCCAGGT GAGAGGGCTG 36801 GTGCCACTGA GGCATCAAGC AGAGGTTTGA GATCTCCTTG GTGACAGTGT 36851 AGAGCAGACA GGTAGATTTG GGAATTTAAG CTTAGACTCA CGTTGGAGAC 36901 TGAGATAGCT CATCTGAGAG GCACTCAGGG CCTAATCTCA GGCAGTAATT 36951 TTAGGGATGT AGGGGAAGAG ATGGATTCTG CACATACTTG GGAGGCTTGT 37001 GGAGGAGTGG GGAGGGAGGC ACAGGGAGGA CTCCAGGGTG GTTCATACGG 37051 CTCCCTGCTT CTGTTCCTGT CCCCCTTTGT CAAGCTGTGG TCTGTACTGC 37101 GTGTTCCATC TTGTTTCTAA GCTGCTTTTG CCCAGTCTTT CCAGCATTTC 37151 CCTTTCGTCA TGTTAGTCTG TGCCTGTCTA CGTGAACTAT GGTGACGTTT

37201	ATTGGGCCTG	GCACTGTGAG	GTGCTGGGGA	TGTGAAGATC	ATTGTGGCTC
37.251	AGCCGCTGCT	CTCGAGGGCC	TCTGGGTGCA	GTATGCACAC	CTGTGCCTCC
37301	TGTTTGCTCA	GGAAGACAGG	CTTTGAGATG	AGCTGGGGCT	GACATCCCCA
37351	CCTTATCATT	GGGATGGCTT	TGGGTAAGTT	ATGTTCATGT	TCTCTGAGCC
37401	TCCCTTTCCT	CATTGGTAAA	ATGGGTATAA	AATACCTGCC	AGTGGAGGGT
37451	TGTTGTAAGT	AGCCATGGAA	AATGTAAAGC	ACATAGCACT	TACCATTTTT
37501	TCCTGTGTCT	TTAACAGATT	TATCATAGAA	TCCCCGACTC	AGACCCATCT
37551	TCTAGCAAAA	CAAGGCAGAT	CATCTCCACC	ATCCGGACGC	AGAATCTTCC
37601	CAACTGTCAG	CTGATTTCCC	GAAGCCACTA	CTCCCCCATC	TACCTGTCGT
37651	TTGTCATGCT	TTTGGCTGCC	CTGAGCTGGC	AGTACCTGAC	CACTCTCTCC
37701	CAGGTAACAG	AAGACTATGT	TCAGACTGGA	GAACACTGAT	CCCAAATTTG
37751	TCCATAGCTG	AAGTCCACCA		TTACTTTTTT	TCTTTAAGGA
37801					TCCCTAAAAG
	AACGCTGTGT	•	TTTAGGAAAG	TGAAATGCAG	GTGAGAAGAA
	CCTAAACATG			CCAGCAACCT	GTCCTTGTGG
37951		CTGTGCTGCT		GGCAGAGCAT	TCAGTGCCAC
38001		AAGTCGCTGC		GTCATGAGAT	CCTACTTAGT
38051		CTAGAATGAT		ATTTAATTTG	AAGCACCATT
	TGAATGTTCG				CTGTTCGGCT
38151			GTTTTCTTTA		
38201		TATGGTTTAG			AAGAATGCAA
	ACTGCCTTTT		GCTGGGAATA		TATTCTCGTA
38301		AAGGAGTTTA			
38351		GAAGATTGGT			TTTGAGATTT
		GAAGATTAATT			
38401				TGTCAAGTAC	AGTTCGCTTG
	AAAGCCTGCC				
38501		TGGCTCATGC			GAGGCTGAGG
38551		ACGACATTAG			TAACACGGTG
	AAACCCCCGT				CGTGGTGGCG
38651		GTTCCAGCTA			
38701		GCGGAGCTTG		AGATCGCGCC	ACTGCACTAC
38751		AACAGAGCGA			AAAAAATTGT
	AAAAAAAAA				
38851		NNNNNNNNN			NNNNNNNNN
38901		NNNNNNNNN			NNNNNNNNN
38951		NNNNNNNNN			NNNNNNNNN
39001		NNNNNNNNN		NNNNNNNNN	NNNNNNNNN
39051	NNNNNNNNN	иииииииии	NNNNNNNNN		NNNNNNNNN
39101	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNN
39151		NNNNNNNNN		NNNNNNNNN	NNNNNNNN
39201	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39251	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39301	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39351	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39401	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39451	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39501	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39551	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39601	NNNNNNNNN	NNNNNNNNN	NNNNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39651	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39701	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
39751	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNNN	NNNNNNNN
39801	NNNNNNNNN	ииииииииии	NNNNNNNNN	NNNNNNNNN	NNNNNNNN
39851	NNNNNNNNN	ииииииииии	NNNNNNNNN	NNNNNNNNN	NNNNNNNN
39901	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNN
39951	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN .
40001	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN
40051	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	(SEQ ID NO:3)
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#### FEATURES:

Start: 2058

2058-2156 Exon: 2157-7996 Intron: 7997-8094 Exon: Intron: 8095-8869 Exon: 8870~9053 Intron: 9054-25147 25148-25339 Intron: 25340-29365 Exon: 29366-29542 29543-30639 Intron: 30640-30792 Exon: Intron: 30793-37517 Exon: 37518-37736 37737 Stop:

#### CHROMOSOME MAP POSITION:

Chromosome # 8

#### ALLELIC VARIANTS (SNPs):

WILDERIC A	WUTWIT	(SNES):				
DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
825	G	A	Beyond ORF(5	')		
2632	С	T	Intron			
4430	С	T	Intron			
4791	С	T	Intron			
4886	G	С	Intron			
4887	A	T	Intron			
4889	${f T}$	Α .	Intron			
5110	G	T	Intron			
6911	G	Α	Intron			
7212	A	G	Intron			
7355	С	${f T}$	Intron			
7398	T	С	Intron			
7653	T	С	Intron			
8310	A	G	Intron			
8145	С	${f T}$	Intron ·			•
8031	G	Α	Exon	45	R	K
8462	G	С	Intron			
8873	С	${f T}$	Exon	67	N .	N
9190	С	${f T}$	Intron			
9311	${f T}$	-	Intron			
9847	T	С	Intron	•		
10460	С	${f T}$	Intron			
20204	G	A	Intron			
20362	C	A	Intron			
21166	G	Α	Intron	•		
21477	G	A	Intron	•		
22230	С	T	Intron			
22941	A	G	Intron			
23963	С	T	Intron			
25686	A	C	Intron			
26018	A	G	Intron			
26078	G	A	Intron			
26625	С	G	Intron	•		
27151	С	T	Intron			
28032	G	A	Intron			
28772	G	A	Intron	•		
29572 -	C	T	Intron			
29761	C	T	Intron	•		
30732	G	C .	Exon	281	L	L
				•		

FIGURE 3N

30841	G	${f T}$	Intron
31376	G	A	Intron
32032	A	G	Intron
32525	A	G	Intron
34179	G	T	Intron
34249	T	C	Intron
34451	T	C .	Intron
34532	T	С	Intron
36541	T	· C	Intron
36607	Α.	G	Intron
36681	A	G	Intron
37493	С	T	Intron
37966	С	A	Beyond ORF(3')
37973	T	C	Beyond ORF(3')
38113	С	, A	Beyond ORF(3')
38298	G	С	Beyond ORF(3')

#### Context:

#### DNA Position

825

GCAGTGAACGTACCTGACAGGTTTCCTGTTTGTTTTTTGAGATGAAGTCTCGCTCTTGTCC CCCAGGCTGGAGTGCAATAGCGCGATCTCAGCTCACCTCCAACCTCTGCCTCCTGTGTTCA AGCGATTCTCCTGCCTCAGCCTCCCAGGTAGCTGGGATTATAGGCGCCTGCCACCATGCC TGGCTAATTTTTGTATTTTTAGTAGAGACGCAGTTTCAGCATGTTGGCCAGGCTGGTCTT GAACTCCAGACCTCAGGTGATCCGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGC [G, A]

(SEQ ID NO:7)

(SEQ ID NO:8)

GGCCTTTTTTTTTTTTTTTTGAGGGGGGGGTCTCACTCCATCGTCCAGGCTAGAATGCT
GTGGCCTGAACATGACTCACTCCAGTTTTGACTTCCTTGGCTGAAGCCATCCTCCACCT
CGGCTTCCTGATCCCGAGTAGCTGGGACTCCAGGCACGTGTCACCAATGCATGGCTAATT
TTTAAATTŤTTTTGTAGACACAATGTCTCGCTGCATTGCCCAGGCTGGTCTTGAACTCCT
GAGCTCAAGCGATTTTCCCACCTCAGCCTTCAAAGTGCTGGGATTACAGGTGTGAGCCAC
[C.T]

GCACCCAACCAGTTTCTCTCTGCAAACTAGGGAAAAAATTTACGCTTAGCAGATATTGAG GGCTGATTATTTCTATCACAGAAGCATTTGGCTATAGAATTTCAGGGTTTAGTAAACTTG ATTTACACTGAATTTTTAGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT TGTGTGCATCACCCAAAAGCCGAGAGTAATGGAAAGAGCAGGCTGTTAGTAATCAGGCA GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT

(SEQ ID NO:9)

4791 GGCTGATTATTCCTATCACAGAAGCATTTGGCTATAGAATTTCAGGGTTTAGTAAACTTG
ATTTACACTGAATTTTTAGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT
TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGAGCAGGCTGTTAGTAATCAGGCA
GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT
AAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAACCTTGGTAACTTAACCTCTGAAC

FIGURE 30

	·	
	[C,T] ACAGTTACTTCATCTGTAAAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAACT TCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTTGAGTGTTTTGGCTCAGAATCACTTGGC AGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTT GCTAAAGAAATAATTATGAGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTAT	(SEQ ID NO:10)
	TGCCTATTTTCTAAAACACTAAAAATGCTAAATTCTGCCCCAGGTCTTGCCACAGATGTT	(200 ID MO:10)
4886	CTACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAA AGAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTT AGACTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAAC AACCTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAATAGGGATGTATGT	·
	TGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT	
	TGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTG	(SEQ ID NO:11)
4887	TACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAA GAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTA GACTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACA ACCTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAATAGGGATGTATGT	
	GTGTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCA	(SEQ ID NO:12)
4889	CGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGA GCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGA CTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAAC CTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAATAGGGATGTATGT	
	GTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCA	
	TTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGATA	(SEQ ID NO:13)
5110	AAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAACTTCCCAACTCTAAGATGGT CTGAAAAGAATTTTTTGAGTGTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAA GTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTTTGCTAAAGAAATAATTATG AGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTATTGCCTATTTTCTAAAACA CTAAAAATGCTAAATTCTGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCT	
	[G,T] TGAGACCTTAAAGGGTTGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCA TGGAGTTAAGTGCTTGATAAATGGTGGTTATCAATCTGATTATGTAAATT CAGTTCTCAAGTTTGTGGTTTTTTTCCCCTCCTGGAGAAATCTATTCTATTTTAAAGTGA GGAAGGCTCCGTGGAGGGCTGGTAGCTGGTAGCTGTTCACTTGTGGAACTTTCAGCCTGA GGCTGGAGCCCCTTCCTGGGAGTCTGGTCTTGTCGTCTTCCTGACCACCCCCACACCCTT	(SEQ ID NO:14)
6911	CCACCTTGGCCTTCCGAAGTGCAGGGATTATAGGCGTGCGCCACTGCACCCGGCCCTGTT GGATAAATGATTCCAGTCTCTCCCAAAAAGAACTGTTGTAAGACTGTGGGGTGAGGGGAG GGAAGGGACAAATAGGAACCCGCCGTATTTTCCACTCCCTGTGGGCCTAAAACTGCTCTA AAAAATAGTCCATGAAAAAAATACATAGTACAAACAGCAACTCTTTCTGATATGCTTGCAT TTAAAATCAGGCTTTTTCTCCCTTTTGGAAAAAACACAGTCCTTGTTTGCTTTAGGGAAGA [G, A] TAAAGGTCAGTGCGCTGCATTGCATTAATTTCGAAGGGAAAGATGAGAAGACATCTTGAA	·

FIGURE 3P

	AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTCAGAAAAAACTACTGCAGTAAG AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA TGGCGGGGGGAGCCGGATGTCAGTGGAAAATTATTACGAGGAAACACAGGGGTGTGC	(SEQ ID NO:15)
7212	TAAAGGTCAGTGCGCTGCATTGCATTAATTTCGAAGGGAAAGATGAGAAGACATCTTGAA AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTCAGAAAAAACTACTGCAGTAAG AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA TGGCGGGGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGC [A, G]	
	TTCTTGCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGG AACCTAATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAA TTTAGCAGGATTCTTGGTAAAACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTC CAGGCTTTATTGGGAAGAGGATTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACT CTGTCACTGGGAGGACGAGCGAGCCGCTCGGAAGTGCGTTCTCTTAGCGGCCAGT	(SEQ ID NO:16)
7355	CAAAACAGATTTTATTCAGAAAAACTACTGCAGTAAGAGAGAG	
	TCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGCGAG	(SEQ ID NO:17)
7398	GAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGG GGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGCATTCTT GCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCT AATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAG CAGGATTCTTGGTAAAACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGC [T, C] TTATTGGGAAGAGGATTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCA	
	CTGGGAGGACGAGCCGCTCGGAAGTGCGCTGGGTTCTCTTAGCGGCCAGTGGGTTC TGGTGAGAAGGGCAACAGCGGGAGGAGGCGCGGTGCGGAGCCGGGAGGCCGGGGCCGGG CTGCGGGGCTGCGGGCCCGTTGTGGGTCGGCCCAGCGCGTATTCGAGTAGAGGGC GAGCCCGTCCCGCCTCTCGTCGGGCGCTTCCCAGATCTGCTTGAGTCTATGGAGGAAAAA	(SEQ ID NO:18)
7653	AACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGG ATTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGC GAGCCGCTCGGAAGTGCGCTGGGTTCTCTTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCA ACAGCGGGAGGAGGCGCCGGTGCGGAGCCGGAGCCGGGGGCGGGGCTGCGGGGCTGCGG GGCGGCCCGTTGTGGGTCGGCCCAGCGCGTATTCGAGTAGAGGGCGAGCCCGTCCCGCC [T,C]	
	CTCGTCGGGCGCTTCCCAGATCTGCTTGAGTCTATGGAGGAAAAACTCCGCGGGGTCCGC GATTCCCATGGCCGCAGCCGCTGCGGCACCAAGGCCATGGCCCTCTTCAAGCGCACCTT GGTGCTGAGTCCCGCCGCGGCGCCCAGGGGCCCGGGGCGCAGGCACCGCCCCGCGGGGCTG CTGCTTGCCTCCTGCCGCCTGGCCCTGCAAGGACTGGCCTCGGGGAGAGGGCGGCAGGCT GTGGAGCCGCCTGCCCCAGTCCCAGTCCCACTCCCACTCCCACTCCCACTCCCACTCCTG	(SEQ ID NO:19)
8310	CAGCCTGAAAACTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTAT CCAGGCGCTGGATGGGGAAATGCGGTGAGTGATGGAGGCAGCCCTCTGGCTTGGAGGAA AGCTTGTCCGGGACTTTTGAGTGTTTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTG CAGCCTCGTTGCTGTGGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAA GCCCTTCCAGGCTCTTTGCCATCTAGTAGAGTCCCTGCGGGCCCAGCCTTTCAGAGAAG [A, G] GGGGGGAGGGGGTGATGTTTATTAACTTTTTTTAGTCTTGGCAGCTGAACCTGCCTG	
	GCAGGTCGTGTATTTCTCGGCTTCCCTTATCCAACTTTGCATTTCTATTTCTAGCATATT GGGTTGATTCTTTTGAAGCTGCCTCTGTGCACATTACACCCATGAACTTAGACCAGTTGC	

FIGURE 3Q

	CTTTATGTATGATCGTATTTATACTGAGAAGTTACTGTGTTTTTTTGACTTTCTAT TTGCTACATATTAGTTCGGTCTAAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTG	(SEQ ID NO:20)
8145	CAGCCTGAAAACTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTAT CCAGGCGCTGGATGGGGAAATGCGGTGAGTGATGGAGGCAGCGCCTCTGGCTTGAGAA AGCTTGTCCGGGAC [C,T] TTTGAGTGTGTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTG GGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCCAGGCTCT TTGCCATCTAGTAG (SEQ ID NO:21)	
8031	CAGCCTGAAAACTTGCTACA [G,A] GTATCTCAATCAGACCAGTC (SEQ ID NO:22)	
8462	GCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGTGGCTTATCCAGAACAT AGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCCAGGCTCTTTGCCATCTAGTAGAG TCCCTGCGGGCCCAGCCTTTCAGAGAAGGGGGGGGGG	. (SEQ. ID. NO:23).
8873	AAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGG AGTAGTGGTGACATTCAACTAGTAGGCTTTTTAATAAACTACAGAAGTTCATTACTCTCA TGTAAGGAAGGAAAACTAATGTAACTTTCGTTAAGTATGAAAAGCGTTGGATATCCTTAT AGTTCTTTAGAGTTAAGGGTGAGATGGGTTTAGAAAGTGGCCAGGCACAAGTTATTTTAA AATAAAAAATCTTTGGCTGTTTGTTCCAATATATTAATAGTTTTCCCTTTTTTACAGCAA [C, T] GCAGTGTGCATATTTTATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACACACAC	(SEQ ID NO:24)
9190	ATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACCATCAGTGTGGAAAAGA AGGTCCCGCTGTTACACAACTTTCACTCTTTCCTTTACCAACCA	(SEQ ID NO:25)
9311	GAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGCA TCTTGTCTACGGACTGTTGTGTTCATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATAC ATGTGGAGAAAGGTTAAATAAGCATTCTGAGGCAGCATAATGTGAGGGTTAAAAACTCC GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG [T, -] AATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACGTAGGTAATGCTC TTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTTCTTCCTGTGG GAAGACGCAGTCAAAATTTTAGTGTTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTGC CGACTGTATGATGCAGCCTACCTGTAACACTGCTGGCCTCTTGACTACCCGGAGCCTGGT AGCATGGGACTGCTCCACGATGGGCAGCCTGGCATGGGGGGCGGTGTCTTTGGCA	(SEQ ID NO:26)

FIGURE 3R

9847	CTGGTAGCATGGGACTGCTCACGATGGGCAGCCTGGCATGGGGGGGG	
	AAAGTACTTAGTGCCTGGTACAGGGTAAGTATTCTGTAAGTATTAGCTATTTTGGTCTATT TTGTTGGAGTAAAGTGGGTTATAGTTAAAATCCTAAGATTTTTAAAGTCCCTCAAGTTCA [T,C]	
	GTGGACATCTGCCTAGGTCCTACTATCCTAGAATTCGCATGTCTTATCACACAAATAACT GATTCTTCCATATCTTATAAATAAAGGTTTGATTTAGCAAAGTCACATGTTGTGTAATAG	
	CTCGAAGAAGCCCTTTTTGTCCACAGTTGCCAGAGCTTTTTGGAGAACAGTCCTTATGTTA TTGAAACAAACCTAATCTGTAGCTGAGTTGGGAGGGAGCTAAGTGGACAGAGAGTCCTCC	(000 75 370 07)
	ACCCAAACAAAAGAATCTTTGATTCTTGGGCATAATGGGAGCAATATTTAAAAAAAA	(SEQ ID NO:27)
10460	AGGAATGTTTGGGGAAGACTCTTGCGGTGCAAAGGCTGTTTCAGATTGCTGAGATCAGAC CTTAAGTACCAAAGCCCAAATATAGTACAACATAATACAAATGAGAAGAAAATAGCTGAA GAATAATTCGAGTTTATACAGTACAATTCAAGAGAAAAAAAA	
•	TGGGTGAGAATTAGAACTGTAACCCTGGGAAGGTCCTGGTGATTTGACTCTCACAGGACA CCTGATGACCAGAGGATGGGTTTCCTTTGATGGGAAATCTGTGGCGATTCATTGATGGGC	
	[C,T] TCTGAATTCTGCTGAAGCAGGAAGTAGTAATACCCCATTTATAATGGAAGTGCATTCT	
	CACTTAAAAACAACTAATATTATTCTAGCTGGACCTAGCCTCTAGAAACAGCCAAATTAC ATTTGACTTGAGTGGATTCATAATAATTAAAAAAATTTCTGGGGCATGGGATAAATGTGTT	
	AGGTATTGCTAAGTCAAGGCAGCCCTATCCCCTCAGCAGAAGTGAGGGAATATGAAAGTG TGTGAATGCTAACATAATTTTGGGGAATATCGCCGTCAGATTTCCAGATGATATTCCAAC	(SEQ ID NO:28)
20204	TCTGCCAGTTGCGAAGACTGGGAAAAGCACAGTATTTGGGCAGAGTATACTGTTCCTCCA	
	GGTACAGTCACTCACGCCTTTCCTTGGCTAGGAAAGGGAAATCCCCTGACCCCTTGCACT	·
	TCCTGGATGAGGTGACGTCCTGCCTGCTTTGGCTCACCCTCCATGGGCTGCACCCACTG TCCAACCAGTGCCAATGAGATGAACCAGGTACCTCAGTTGGAAATGCAGAAATCACCCAT CTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGCTGTTCCTACTGGGGCATCTTGG	·
	[G, A] AGCAACTCTGGGTCTGAGTTTCTGTTTGTTGCCCTGATGTATATCCCCAGTGCCTAGAAT	
	GATACTTGTTACATAGGAAGTGCTTGATCCATGTTTGCACAAATGAATCTTTCTCATAAT GAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACTTACACCCAGCTTTATGTTGAAGCAT	
	CTCATTATACATTGGAAAGATGAAATGTGTGGGGACTTTGAATCTTCTTTTGAATCTA GAAACATTAGCATTTTTAGACCATTCTATTTTAATATTTTATGAAATTTATGAAATAATAA	(SEQ ID NO:29)
00060		(500 10 10.23)
20362	CCTCCATGGGCTGCACCCACTGTCCAACCAGTGCCAATGAGATGAACCAGGTACCTCAGT TGGAAATGCAGAAATCACCCATCTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGC TGTTCCTACTGGGGCATCTTGGAAGCAACTCTGGGTCTGAGTTTCTGTTTGTT	
	TGTATATCCCCAGTGCCTAGAATGATACTTGTTACATAGGAAGTGCTTGATCCATGTTTG	
	CACAAATGAATCTTTCTCATAATGAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACTTA	
	ACCCAGCTTTATGTTGAAGCATCTCATTATACATTGGAAAGATGAAATGTGTAGTGAGAC TTTGAATCTTCTTTTGAATCTAGAAACATTAGCATTTTTAGACCATTCTATTTTAATATT	
	TATGAAATTTATGAAATAATAAGAAACATGAGGCCGGGCTCAGTGGCTTATGCCTGTAAT CCCAGCAGTTTGGGAGGCCAGGGCTAGTGGATCATGAGGTCAGGAATTTGAGACCAGCTT	
	GGCCAACATGGTGAAACCCCACTTCTACTAAAAATATAAAAATTAGCTGGGCGTGGTGGT	(SEQ ID NO:30)
21166	TAATTCCGCCATTGTTTGCCTTGTGATCTTTGGTGCCATGTCTGTACATATTTCATGATT TCTGTGTTTTTACGGTTTCCATTTCAGATCTCCCTTGAGTTTAGAAATCTGGCTGAGAAA	
	TACCAAACAGTGATTGCCGACATTTGCCGGAGAATGGGCATTGGGATGGCAGAGTTTTTTG	
	GATAAGCATGTGACCTCTGAACAGGAGTGGGACAAGGTTAGTCTCATAAAACAGTGTCTG TGTGTGATGTATTAGACAGAGCTGGCAGTCCTCATAGTGAAGCTCAGAACAAGAAAAGTT [G,A]	•
	TCCAGTATTTTCAGCCCCTCTGGTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCA	
	TAAACAGTTTATTCCAGAGTTAATTCCAAACCAGCAGCTATGTAGGATATCAGCCAGGCT AGGAGTAGGGTACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAG	
	ATTAAAACTACACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCTATTTTTCATAGGA ATGGTGTTTGTGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTA	(SEQ ID NO:31)
	,	

 $\tt TCAGCCCTCTGGTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCATAAACAGTTT$ 

ATTCCAGAGTTAATTCCAAACCAGCAGCTATGTAGGATATCAGCCAGGCTAGGAGTAGGG TACTGGAGAGAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAGATTAAAACTA CACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCTATTTTTCATAGGAATGGTGTTTG [G, A] TCAGATTTAGCAGGCAGAGACATTTCAGACATCTAAAGTGTTGATGTATTTCATACCTTT **AACTGTGCTTAAATTAGGATCTCCGAAAAGATGCTGCTACATGGTCACTACGTTAGTGTA** GGTCCAAGGTCTTGGGCCTCTTAATTTTTCAAACCTCAAAACTTGACAGCAGTTATCTTT GGAACTGCTGATTTGTGCTTCCTAAGTTAACAGCATACAATGACTGCTAGAAATCAATTT CTGCATTTAAGGTGAAGTTAGCCGGGTACTATGGTTTACCTGTAATCTCAGCACTTTGGG (SEQ ID NO:32) 22230 GGATTGCTTGAGCCCAAGAGTTGAAGGTTGCAGTGAGCCATGATTGTGCCACTGCACTCC AACGTGGGTGACAGACAAGACACCTACTGAAAGAAAATAAAGTTGAAGTTAAAACTTCT GGCCAAGAACCAGCACTGGTTATGATAGTAACTCATTTTCTGTTGTGCAGATTTATTCAG GAAACTTAATTTTAGGTTGTTGAATAGAAGTTTTGATCAGATAAAATTGAATTAAAAAAA ATTTTTTTTGAGACAGGGTCTTGCTGTTATCCAGGCTGGTGTGTAGTGGTGTGATCACGG [C,T]TCCCCGCAGCCTCAACCTCCTGGGCTCAGGTGATCCTCCCACCTCAGCCTACCGAGTAGC GGTTTTGCCATGTTGCCCAGGCTAGTCTCAAACTCCTGGCATCAAACAGTCCTCCCACTC TGGCCTCTCAAATGTTGGGATTACAGGCATGACCAGCCAATTATTTCAAGGAGTTATTTT TTTTCTTCTACTTTGGGGGAAGATGAATTATATAAGTCTCCATTTTAGGAGTATTTCTAC (SEQ ID NO:33) AATTTCTGTCTACCTAATTTCAGCAAGATTTCACTCTTTTCATGTTACTTTTGTCCCAGA 22941 ACAAATTTCAAGTGCTTTCTCTTCACCTGTGCATTCTCCCCCTGATTAGTCTCTGGCTT TGTAT.TACTTTCAGTCAGAGACGACTTTTTTTTTTTTGAGACAGGGTCTCACTCTGTCACC CAGACTGGAATGCAGTGGCACAGACAAGGCAGCCTTGACCTTCTGGGCTCAAGCAATCTT CCTTGCCCTCAGCCTCCTGAGTAACTGGGACCACAGGCACGTTGCCACCATGCCTGGCTA [A,G] TTTATTTTAATTTTTTTTTTTGAGACAGGGTATTGCTCTGTCACCCAGGCTGGAGTG TAGTGGCATGATCAAGGCTCACTGCAGCCTTCACCTCCTGTGCTCAAGCAGTCCTCTCAC CTCAGCCTCCCCATTAGCTGGGACTATAGGTCCACACCACTACACCAGGCTAATTTTTGT AATTTTTTGGTAGAGACAGGGTTTCATCGTGTTGCCTAGGCTGGTCTTGAGCTCCTGGGC TCAAGCGATTCACCTGCCTTAGCCTCCCAGGTGTGAGCCACTACACTCAGCCTTTTAAAA (SEQ ID NO:34) 23963 ATACTACCTAGTTTTGAACTCTTAGCCCCTGCCACAGACACGGCAGCCCCTTGAACCTTC CTGGGTTCAAGCGAGCCTCCTACTTCAGCCCCCTGAGTAACTGGGACCACTGGCCTGTGT CACTGTGCCTGGCTAATTTTTTTTTTTTCCTCACATGGGCAATGTTGGGCAAGTTAAATC GACTTCTTTGTGCCTCAGTTTCCTCATCTGAAATGGAGATCATACTGCTATGTACCTGAT [C,T]GGAGTCTCACTCTG (SEQ ID NO:35) 25686 CTGAAAAATCCTTTAACTCTTGTGGTTGCGGGTGACAGAAAAACAAGCCAGGCCTCCCCC AGGCAGCATAAGGGGATGTGGAAAATAGGATAGATTGACATGAGTTTGCTTCAGGTAGAC TGGCTGACTCCCAGGATTCACACCACGTAATCAGTATATTCAAGCCTTGCTGTCCTTGAT TTCTTTCAGACGGTCTTTCTCCAAGTGGTGGATATGGTAACAACCCACGTGCACTAGCTT AACAAAAGTTCTTAGGAATGGCTTTGTTCGGCCTGGCGCAGTGGCTCATGCCTGTAATC CAACAGTTTGAGAGGCCAAGGTGGGCGGATCACCTGAGGCCAGGAGTTCGAGACCAGCCT GGCCAACATAGTGAAACCCCGTGTTTACTAAAAAATACAAAAATTAGCCGGGCGTGGTGG CAAGGGCTTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG AAGCAGAGATTGCGGTGAGCTCAGATTGTGCCACTCCAGCCTGGGCGACAGAGTG AGACTCCCTCTCAAAAGAAGAGGAAGGGCTTGGTTCTTCTGCTCAGCCCTGAATCAGTTA (SEQ ID NO:36) ACCTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAACATAGTGAAACCCCGTGTTTACTAA 26018 AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCCAGCTACCTGGGAGG CTGAGGCAGGAGATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC

FIGURE 3T

 ${\tt CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAAGAAGAAGAGGAAGGGCTTGGTTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGCTGAGTTCTCTGGCCTC}$ 

[A,G]

	GCAGGAAGGGAAAGGGATGGCAGGTAGACAAAAACTCCAGGTGTCTGTAATAAGGGACA GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTTGTT CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTTACCTTTT GCTTTCCATAAAAGTGTTTCCTGCAGCCAAGTACTTTAAAAGTTTTAAAAAGACGGGTGAG	(SEQ ID NO:37)
26078	AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCCAGCTACCTGGGAGG CTGAGGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGTTGCGGTGAGCTCAGATTGTGC CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAAGAAGAGGGAAGGGCTT GGTTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGGTGAGTTCTCTGGCCTC ACCTGGATTACGTCTACACAGTACACACAGAATGGATTTCCCCCAAAGAAAG	•
	GCAGGAAGGGAAAGGGATGGCAGGTAGACAAAAACTCCAGGTGTCTGTAATAAGGGACA GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTTGTT CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTTACCTTTT GCTTTCCATAAAAGTGTTTCCTGCAGCCAAGTACTTTAAAAGTTTTAAAAAGACGGGTGAG GCTAAGTGTGGTGTCTCATACTTATAATCCCAGTGCTGAGGCCAGGAGTTCAAGACCAGC	(SEQ ID NO:38)
26625	TGTGGTGTCTCATACTTATAATCCCAGTGCTGAGGCCAGGAGTTCAAGACCAGCCTGAGC AACACAGCAAGATACCATCTCTATAAAAAATTGTTAGAAAATGATTCTGCTGAAAGAGCA AAAATAAAAATTAAAGAAAGTAGAAAAAATAAAACTAAATTTAAAAGATTAACTGGGCAT GTTGGCATGCACCTGTAŢTCCTAGGTATTCGGGAGGCTAAGGCACAAGGATCCCTTGAGC GCAGGAGCTCAAGGTTGGAŤTGAGTTGTAATCACACCACTGCACTCCAGCCTCGGTGGCA [C, G] AATGAAACTGTCTCAAGAAAAAAAAAAAAAGTGACAGAGGGAAACAATATTTGCAATTCATA GAGCAGATACAGGGTTCATATTCCTAATATTAAAAAAAACTTCTAAAAGTTAAGAAAAAG GCCAACTGCCCCACAGAAAAATCTGAAAAGATCCTGAGTCTTACTCCTAAGAAAAATTC ACACTAGATTAAACTTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGTAATCTCAACACTGGG	(SEQ ID NO:39)
27151	TCCTAAGAAAAATTCACATTTAAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGT AATCTCAACACTGGGAGACCAAGGCAGGAAGATCACTGAAGCCAGGGTATCGAGACCAGC CTGGACAACGTAGTGAGACCTTATCTCTTAAAACAAAAC	(SEQ ID NO:40)
28032	AGGAGCAGAGCCCTGCTCTTCTCATTCACTTACTTTATCTGTAAAATAGCATCATTTCTA CCACACGGTGGTGGTGAATAAAATGAGATGAACTTCTAGCATAGAGTGCTTAGTAAAG GTTCTGGACATTTCGTAGTAGTTGAATCATGCCAAATGTGGTCCTAGGTGATTGGCTTCT TTTGCTAGCATGTTTTCAGGGCTCCTCCATGCTGGGGCATTGCATCACTGCTTTATTCCT TTTTATCGCCTAGTATTATTCCACTGTGTGGATAGACCACATTTATCCATTCATCAGTTG [G, A] AGGATATTTGGGTTCTTCCCATTTTTTTTTGGCTATGGTGAATAGTACTGTGTACATTTGC ATATAAGGTTTTTGTGTAGATGTGTGTTTTCCTTTTTCTTGGGTCTATGCTGAGAAGTGGA ATTGCTGGTTCATACAGCAGCTCGAACCTTGTGAGAGGTCCCAGACGCTTTTCCAAGGT CGCTCCACCATTTTACATTCCCGTCAGCAGTGTGAGAGTCCCAGTTTCACCAGCACTTGT TGTTATCTCTTTTTAACTGTATGTATATATAACATTTTATTTA	(SEO ID NO:41)
28772	AAAAATCATCAAGCCGAATCCCACTGTTAGAATTAAAGGTTTTATTTCACTTTCAAGTTA TCAGGATCCAGGGAGGTGTAATACACTTAGAGGATAGACTCAGCTCATTTCCCAGCTATG CCTTTCAGCAGCATTCTTACCAGAGTAGGAATATAATGTTAGTCATTATTTAGAGGCCTG GCCATCTTGAGAAGGTTTACTGTTTAGTCTGCAGTACAATTATAACTGTTTTTTGTATATT GGGTTATTTTTTCAGAAGTAGGCCAGTAGCTCTAACAGGAGCCTCTTTAGCCTGAATTC [G, A] TCCAAGTAGTGCAGTGTTGCACTAGTTGTCCCTCGGGACATGCTCCCCAATACGTAACTC ACTTCCAGGTTGCAACTGGACACTTACTGGTAGTCAGAAATAGCTATTGCATGGAGCTTA AAATGAACTTGATCTTCGTGAAAGATGAGTCTGCAGCTAAGAGACCTTTACTGTATATCAT	

FIGURE 3U

	AGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	(SEQ ID NO:42)
29572	TCATAGTTCTTATGCACAAAGACCCTTTAATATTGTTTGT	
	GGGGCTAAAGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATA TGATTCCTTAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCC TTTGCTTCCAGCCACCAAACTCAGCCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAAC CTTCTTTCCGGATTTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCCTCA CAGTTAAGTCAAGGTCTTTGGCTTAGATTTATGGGGAGTGCTGGGTAAAACCTGGGTGAA	(SEQ ID NO:43)
29761 .	ACTGCACCACATCCCAGATGTCATCACCTACCTTTCGAGACTCAGAAACCAGAGTGTGTT TAACTTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATACGGGGCTAA AGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATATGATTCCT TAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCCTTTGCTTC CAGCCACCAAACTCAGCTCAG	
	GGATTTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCCTCACAGTTAAGT CAAGGTCTTTGGCTTAGATTTATGGGGAGTGCTGGGTAAAACCTGGGTGAAGCTGTTATC ATTAAAAAGTCTTCATTAAGCACCTAATTACTGCTGTCCTTTTCCTAGACCCGGCATAAA AAGAACCTGGTCCGGTAGACCTAGCCTCTCAGTATGCTAGGAACTTACACTTTTTAGTTG CCTTTACCAAGTATTGCAGATACTGCAAATAAGTGAAGAAAGTAACAGCATTTAACT	(SEQ ID NO:44) .
30732	ATTCTGTGTGTTGTGAGAAAGGGAGGAGTGGGGAAGGTAAAAATCTTGACATACTTTCT TCGTGGGTATTTTTTCTTGAGCAATCCATCTTAGTTGATTAGCAGTTAGCAATTGCCCA TTCAACAGAAGGTTTTCTTACCTTTTTTGTGATAATGATAGCTAACGACATCATTTCTTCT TTTTTCCCTCTCTTCTTGTTGTCTCTAGGTGATGGCCATTGCCACTTTTGGCTGCCTGTTA TAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAAGGGCAAGCAGTGACCCT [G, C] ATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAGTATATAGGAAGAG GTGGGTTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGATTTAGTAATGTCA CTGTTTAACCAGGTTTGGATATTAGATGATCCTAACAATTCACTATCCTGTGGCCTAAAG AGACAGGAATTGATATCCTTTTATAAGGAAAAAAGTCTATTCACAGGAGCCGAGCAGATTG	
20041	CTCACTGCTGTGTGTGCCCTGGTGAGAGGAGATAAATGGAGCAAGGCTGTAGGTTGGAG GCAATTGCCCATTCAACAGAAGGTTTTCTTACCTTTTTGTGATAATGATAGCTAACGACA	(SEQ ID NO:45)
30841	TCATTTCTTTTTTTCCCCCTCTCTTGTTGTCTTTTTTGTGATAATGATAGCTAACGACA TCATTTCTTCTTTTTTCCCTCTCTCTTGTTGTCTCTAGGTGATGGCCATTGCCACTTTG GCTGCCTGTTATAATAACCAGCAGGTGTCAAAGGGCAGTGAAGATTCGGAAAGGGCAA GCAGTGACCCTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAG TATATGGAAGAGGGTGGGTTTTAATTTAA	·
	GTGGCCTAAAGAGACAGGAATTGATATCCTTTATAAGGAAAAAAGTCTATTCACAGGAGC CGAGCAGATTGCTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCT GTAGGTTGGAGCCCCTCAGTAGAATCATAGATTTTGAGCŢGCAAGATGATGCAGGAGGCC AACCAAGCTTCTTGTTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTGATGCAG	(SEQ ID NO:46)
31376	GAGGCCAACCAAGCTTCTTGTTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTG ATGCAGTGCGTGATTGAGTGGATCTCTGGCTCCCGTCCATGTGTCCTGACACCCAGTCTG GTACTTTCATTATGCCACAGGCCTCAATTGAAAAATCACAGTAGGGAATTTAGGCCAAGG AAAGCCATCAAGTTGCAATTATTTCCTAAATTTTCTTTGGAAAATTTCATTTCAAATACC AAAACCATCCTATAAAAAAGAAAACTTACCTTCTTAGGTCAAATCTCTAATATTTGACTAG [G, A]	·
	TTCAAAAAGTTTATTTCTGGCCAGGCACAGTAGCTTACTCCTGAAATCCCAGCACTTTGG GAGACCAAGGTGGGAGGATCACTTGAGGCCAGGAATTCAAGACCAGCCCGGGCGACATAG CAAGACCCCATTTCTACAAAAAATTTAAAAATTGTCATGGTGGTGCACGCCTGTGGTCCC AGCTACTCAGGAGGCTGAGGCAGGTGGATCACATGAGCCTGAGAGGTCGAGGCTACAGTA AGCTGTGTGATTTCATCATTGCACTCTAGCCTGGGTGATAGAGTGAGACTTTGTCTCAAA	(SEQ ID NO:47)

#### FIGURE 3V

32032	TCTCTAGGCCCTAGAGCAGTGGTTTGTAAATGGAGGTGATTTGCTCCCCCCCC	
	TTACGCGTTTACAGGAATATGGTTTGCAACAGTGTTTTCATCTAAATAGAATTATACAAA ATAGCGATTTCTGATTTCTTTGCATATTGCACATTCTTCTTATACTTCCTCCCTACCTT TATCTGACACAGAAATGCTGTATGTCCAGAACTTCTTATCAGAGGCACCTATGGAAGTCTA AGGGAAGACCACATCGCTTTTAAAAACCCTAAAATTTTGTAGTCACTAGATGAAAATATT CAGCCAGTGACCCAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAA	(SEQ ID NO:48)
32525	ATCGCTTTTAAAAACCCTAAAATTTTGTAGTCACTAGATGAAAATATTCAGCCAGTGACC CAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAACTTACTT	•
	GCACTATTTATTCATTTTATATAAACTAGAAACATTTTATGTAGTAAGTA	(SEQ ID NO:49)
34179 .	CTGCTGTATGTAGCACAGCATTGCACAAGAGCTTATTTCAGTCTAGTAAACATTTATAGG. AGCCTGTGTCATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAAACT TTGGGAGGCTGAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAAT ATGGCAAAACCCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACACT TGTCATCCCAGCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACTCGGGAGGTGGAG [G,T]	
	TTGTAGTGAGCTGAGATGGCACCACTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTT TCTCAAACTCCTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGAAAAGTCGG CTATGACCTGTCCTTGACAAGCAGATGTAACTCCTTGATTGA	(SEQ ID NO:50)
34249	ATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAAACTTTGGGAGGCT GAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAATATGGCAAAAC CCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACACTTGTCATCCCA GCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACTCGGGAGGTGGAGGTTGTAGTGA GCTGAGATGGCACCACTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACT [T,C] CTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGAAAAGTCGGCTATGACCTG	
	TCCTTGACAAGCAGATGTAACTCCTTGATTGAGGCTAGTAGGTTTTTAAGACCTGAATAA TTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTGGTCTAG CAACGAAGCATCTAGAAGGTCTCTTTTGGCCTTACCGGCTCTTTTTAGGTAAGTCCACGT CTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTCATGTTTATATGTTAGAAATGA	(SEQ ID NO:51)
34451	GAGCATCGCTTGAACTCGGGAGGTGGAGGTTGTAGTGAGCTGAGATGGCACCACTGCACT CCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACTCCTCAAGTATTTGGCTTCAACT TTATGCCGGGCATGTAGATGAAAAGTCGGCTATGACCTGTCCTTGACAAGCAGATGTAAC TCCTTGATTGAGGCTAGTAGGTTTTTAAGACCTGAATAATTGAGTTTGCAGAAACCTACT GTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGGTC [T,C]	
	CTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCAGCT CTTCCAGTTGTGCTGTCATGTTTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTT TGCCACTAATTGTATTACCGGGGACTGTCACAACCAAGATTTCTCTTAATTTATTCACCT TACTTATCTCCTGGAAGGGCATATTGAAGTGCTCTTGGAGTTCTCTAAAAGGGTTTTTGT TGGTTGTGTATATTCACTTGGGTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCC	(SEQ ID NO:52)

 ${\tt AGGCCCTTTCTCAAACTCCTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGA}$ 

34532

TTTTTAAGACCTGAATAATTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAAATGGA GAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTG TTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTCATG [T,C]TTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTTTGCCACTAATTGTATTACCGG GTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCCCAAAAGGATGTAAGATGGCTT ATGGTTATAAGTACAACAGGCTAACAAAGTACAAGTAGATGAGAAAGTAAAATGAAGAAA (SEO ID NO:53) GGTAGGAGCCAGTTGAAGGGACGTGGGAGGCGCATTCCAGAGAGAAGGAGTGGTATGAGA 36541 . CTGGAACAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTT TGTTTTTTTTTTTTTTTTGAGACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGG CATGATCTCGGATCACTGCAACCTCCACCTCCCAGGCTCAAGTGATCTTCCCACCCCAGT CCCCAAGTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATT [T, C] TGTAGAAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAG TCTACATGCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCC CGGCAACTGTTACTAGACTATAGAGAGGGGGGGGGGGCAAGGGCTGGTGACACTAGACAGG TGCAGTAGGTCTGGACCATGGGTGGCCTTGCGCTACACATTACAGAGCTCAGGCTTTTTT  ${\tt TCTCCAGGTGAGAGGCCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGG}$ (SEQ ID NO:54) CAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTTTGTTTT 36607 TGTTTGTTTTTTGAGACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGGCATGAT CTCGGATCACTGCAACCTCCACCT.CCCAGGCTCAAGTGATCTTCCCACCCCAGTCCCCAA GTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATTTTGTAG AAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTAC TGCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGGCAA CTGTTACTAGACTATAGAGAGGGGGGGGGGGCAAGGGCTGGTGACACTAGACAGGTGCAGT AGGTCTGGACCATGGGTGGCCTTGCGCTACACATTACAGAGCTCAGGCTTTTTTTCTCCA GGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAG (SEQ ID NO:55) TGTAGAGCAGACAGGTAGATTTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATA GACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGGCATGATCTCGGATCACTGCA 36681 ACCTCCACCTCCCAGGCTCAAGTGATCTTCCCACCCCAGTCCCCAAGTAGCTGGGGGACC ACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATTTTTGTAGAAACAGGGTTTTAC TGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTACATGCCTCAGCCTCC TGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGGCAACTGTTACTAGACT TAGAGAGGGGGGGGCAAGGGCTGGTGACACTAGACAGGTGCAGTAGGTCTGGACCATG GGTGGCCTTGCGCTACACATTACAGAGCTCAGGCTTTTTTTCTCCAGGTGAGAGGGCTGG TGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAGTGTAGAGCAGACAG GTAGATTTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATAGCTCATCTGAGAGG CACTCAGGGCCTAATCTCAGGCAGTAATTTTAGGGATGTAGGGGAAGAGATGGATTCTGC (SEQ ID NO:56) TGACGTTTATTGGGCCTGGCACTGTGAGGTGCTGGGGATGTGAAGATCATTGTGGCTCAG 37493 CCGCTGCTCTCGAGGGCCTCTGGGTGCAGTATGCACACCTGTGCCTCCTGTTTGCTCAGG AAGACAGGCTTTGAGATGAGCTGGGGCTGACATCCCCACCTTATCATTGGGATGGCTTTG GGTAAGTTATGTTCATGTTCTCTGAGCCTCCCTTTCCTCATTGGTAAAATGGGTATAAAA TACCTGCCAGTGGAGGGTTGTTGTAAGTAGCCATGGAAAATGTAAAGCACATAGCACTTA [C,T]CATTTTTTCCTGTGTCTTTAACAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCT AGCAAAACAAGGCAGATCATCTCCACCATCCGGACGCAGAATCTTCCCAACTGTCAGCTG ATTTCCCGAAGCCACTACTCCCCCATCTACCTGTCGTTTGTCATGCTTTTGGCTGCCCTG AGCTGGCAGTACCTGACCACTCTCTCCCAGGTAACAGAAGACTATGTTCAGACTGGAGAA CACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACTTTTTTTCT (SEQ ID NO:57)  $\tt CTGCCCTGAGCTGGCAGTACCTGACCACTCTCTCCCAGGTAACAGAAGACTATGTTCAGA$ 37966

#### FIGURE 3X

CTGGAGAACACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACT TTTTTTTTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTTCCTACTACTTTAATCCCT

AAAAGAACGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAA ACATGAAAGGAAAGGGTGCCTCATCCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTG [C, A] TGCTTGTGGCTCATGGCAGAGCATTCAGTGCCACGGTTTAGGTGAAGTCGCTGCATATGT GACTGTCATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAA TTTGAAGCACCATTTGAATGTTCGTACTAGTAGAAAATGATGTGAATTTTCTTTTCTGTTC TATTTATGGTTAGGTAACAGTTAGATGTTTCCTAAGAATGCAAACTGCCTTTTCCACAC (SEQ ID NO:58) 37973 GAGCTGGCAGTACCTGACCACTCTCTCCCAGGTAACAGAAGACTATGTTCAGACTGGAGA ACACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACTTTTTTTC TTTAAGGATGGATGTTGTTCTCTTTATTTTTTTCCTACTACTTTAATCCCTAAAAGAA CGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAA AGGAAAGGGTGCCTCATCCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTTG [T,C]GGCTCATGGCAGAGCATTCAGTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTC ATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAATTTGAAG ATTTTTCTCATCATTTTGTTTTCTTTAATTGGGTTGAATGGAGTAGAAATATTTAT GGTTTAGGTAACAGTTAGATGTTTCCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCT (SEQ ID NO:59) TCTCTTTATTTTTCCTACTACTTTAATCCCTAAAAGAACGCTGTGTGGCTGGGACCTT 38113 TAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCCTCATCCC AGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGCTTGTGGCTCATGGCAGAGCATTC AGTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTCATGAGATCCTACTTAGTAT GATCCTGGCTAGAATGATAATTAAAAGTATTTAATTTGAAGCACCATTTGAATGTTCGTA [C,A]TAGTAGAAAATGATGTGAATTTTCTTTCTGTTCGGCTCCTATTTTTCTCATCATCTTTGTT  $\verb|TTCTTTAATTGGGTTGAATGGAGTAGATAGAAATATTTATGGTTTAGGTAACAGTTAGAT|$ GTTTCCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATTCTGGGTAT TCTCGTATTCTCATTTAAAGGAGTTTAGCTTTCAGAGAGAAACAGCAGGATTGCTTTTGA CCTTTTAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTTGAGATTTTTATAATAAAGAA (SEQ ID NO:60) 38298 CACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTCATGAGATCCTACTTAGTATGATCC TGGCTAGAATGATAATTAAAAGTATTTAATTTGAAGCACCATTTGAATGTTCGTACTAGT TTAATTGGGTTGAATGGAGTAGATAGAAATATTTATGGTTTAGGTAACAGTTAGATGTTT CCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATTCTGGGTATTCTC [G, C] TATTCTCATTTAAAGGAGTTTAGCTTTCAGAGAGAAACAGCAGGATTGCTTTTGACCTTT TAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTTGAGATTTTTATAATAAAGAATTTAA AGCTCAAGAATGGAGTTGATGGCCCAGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTT GGGAGGCTGAGGCGGTCGGATCACGACATTAGGGGATCGAGACCATCCTGGCTAACACGG (SEQ ID NO:61)